

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: January 17, 2003, 12:46:44 ; Search time 12 seconds

(without alignments)
660.165 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGSGSGRLSKELLAETQDIT.....EFQHVHSRDPFASFRIKL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	191	KIPL_HUMAN	Q99828 homo sapien
2	904	94.5	191	KIPL_MOUSE	Q92074 mus musculu
3	903	94.4	191	KIPL_RAT	Q92100 rattus norv
4	340	35.5	187	KIP2_MOUSE	Q92309 mus musculu
5	338	35.3	187	KIP2_HUMAN	Q75838 homo sapien
6	215.5	22.5	177	KIP2_MOUSE	P42322 naegleria g
7	209.5	21.9	174	CALB_NAEGR	P42322 naegleria g
8	198.5	20.7	174	CALB_SCHPO	P87072 neurospora
9	198.5	20.7	174	CALB_NEUCR	P25296 saccharomyc
10	185.5	19.4	169	CALB_YEAST	P06705 homo sapien
11	185.5	19.4	169	CALB_HUMAN	Q63810 mus musculu
12	177.5	18.5	170	CALB_MOUSE	Q24214 drosophila
13	177	18.5	194	CALC2_MOUSE	Q62877 mus musculu
14	173.5	18.1	170	CALB_DROME	P48451 drosophila
15	172	18.0	194	CA22_HUMAN	Q99653 homo sapien
16	171.5	17.9	186	CALC_MOUSE	Q63811 mus musculu
17	170.5	17.8	175	PREO_DROME	P37236 drosophila
18	169.5	17.7	189	CALC_MOUSE	P28470 rattus norv
19	165.5	17.3	189	NCS2_RAT	P36609 caenorhabdi
20	157	16.4	190	NCS2_MOUSE	Q16981 aplysia cal
21	151.5	15.8	195	APLC_APLCA	Q43745 homo sapien
22	150	15.7	189	H520_HUMAN	P36610 homo sapien
23	150	15.7	189	NCS1_HUMAN	Q91614 xenopus lae
24	145	15.2	190	NCS1_XENLA	P36608 caenorhabdi
25	145	15.2	192	VIS3_CHICK	P42324 gallus gall
26	144	15.0	192	VIS3_MOUSE	P33333 homo sapien
27	144	15.0	192	VIS3_MOUSE	P37235 homo sapien
28	139	14.5	199	VIS3_MOUSE	P43325 drosophila
29	136	14.2	214	NCAH_DROME	P33332 rattus norv
30	135.5	14.2	214	TESC_HUMAN	Q96832 homo sapien
31	135	14.1	192	NCAH_MOUSE	Q91x97 mus musculu
32	134	14.0	192	HIPD_HUMAN	P32076 homo sapien
33	130.5	13.6	172	CATR_MOUSE	P41209 mus musculu

34	130	13.6	192	1	NCAH_CHICK	Q12953 gallus gall
35	129.5	13.5	214	1	TESC_MOUSE	Q91x15 mus musculu
36	129	13.5	192	1	NCAH_HUMAN	P26554 homo sapien
37	129	13.5	192	1	NECX_APLCA	Q16982 aplysia cal
38	129	13.5	791	1	KDGC_HUMAN	Q09719 homo sapien
39	128	13.4	189	1	NCS1_SCHPO	Q09711 schizosacch
40	127.5	13.3	172	1	CAT2_HUMAN	Q12798 homo sapien
41	127	13.3	190	1	VIS1_HUMAN	P26677 homo sapien
42	127	13.3	804	1	KDGB_HUMAN	Q94869 mus musculu
43	125.5	13.1	195	1	H520_MOUSE	P49621 rattus norv
44	123.5	12.9	801	1	KDGB_RAT	Q06389 saccharomyc
45	123	12.9	189	1	NCS1_YEAST	

ALIGNMENTS

RESULT 1
KIPL_HUMAN
ID KIPL_HUMAN STANDARD: PRT: 191 AA.
AC Q99828; 000735; 000693; 099971; Q96354;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE interacting protein 2-28) (STR2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-98040126; PubMed-9372844;
RT Wu X., Lieber M.R.;
RL "Interaction between DNA-dependent protein kinase and a novel protein,
KIP.";
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE-Fetal liver;
RT MEDLINE-97184102; PubMed-9030514;
RL Nalk U.P., Patel P.M., Parise L.V.;
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE-20284952; PubMed-10826701;
RT Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RL "Genomic structure of mouse and human genes for DNA-PKcs interacting
protein (KIP).";
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE-Cervix;
RT Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191;
RA MEDLINE-20283154; PubMed-10822252;
RT Hwang P.M., Vogel H.J.;
RL "Structures of the platelet calcium- and integrin-binding protein and
calcium-regulated recognition; homology modelling and NMR studies.";
J. Mol. Recognit. 13:83-92(2000).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

Fri Jan 17 13:03:43 2003

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CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL; U83236; AAB39758.1; -
CC EMBL; U85611; AAB53387.1; -
CC EMBL; U82226; AAC51106.1; -
CC EMBL; AB021866; BAA36281.1; -
CC EMBL; BC000846; AAB00846.1; -
CC PDB; 1DGV; 08-DEC-99.
CC Genew; HGNC:16920; CIB1.
CC MIM; 602293; -
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 2.
CC ProDom; PD000012; EF-hand; 1.
CC SMART; SM00054; EPH; 2.
CC PROSITE; PS00018; EF_HAND; 2.
CC Calcium-binding; Repeat: 3D-structure.
CC CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
CC CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
CC CA_BIND 172 172 T -> S (IN REP. 3 AND 5).
CC CONFLICT 44 44
CC SEQUENCE 191 AA; 21717 MW; 9AA6EA78978E155 CRC64;
CC -----
Query Match 100.0%; Score 957; DB 1; Length 191;
Best Local Similarity 99.5%; Pred. No. 4.1e-69;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC 1 MGGSGRLSKELLAEVQDLFTLTKQELLAHRRFCLEPQORTVYESSLRQVPEQILS 60
CC |||||
CC 1 MGGSGRLSKELLAEVQDLFTLTKQELLAHRRFCLEPQORTVYESSLRQVPEQILS 60
CC
CC 61 LPKLKAPKERICRVFTSPAKSLSEDFDLDSVFSDDTATPKSHYAFRIEFD 120
CC |||||
CC 61 LPKLKAPKERICRVFTSPAKSLSEDFDLDSVFSDDTATPKSHYAFRIEFD 120
CC
CC 121 GTLNRLXRLNCLTGEEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISR 180
CC |||||
CC 121 GTLNRLXRLNCLTGEEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISR 180
CC
CC 181 PDPASFVKIVL 191
CC |||||
CC 181 PDPASFVKIVL 191
CC
RESULT 2
ID KIPL_MOUSE STANDARD; PRT; 191 AA.
AC QZ0F4; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKCS
DE interacting protein) (kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;

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RX MEDLINE-99069785; PubMed=9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohhira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 19q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization.";
RL J. Hum. Genet. 43:275-277(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-Fetal kidney;
RX MEDLINE-99160477; PubMed=10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
RL Mamm. Genome 10:315-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RX MEDLINE-21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Ganiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB006463; BAA74429.1; -
CC EMBL; AB017361; BAA36165.1; -
CC EMBL; AF173010; AAG38960.1; -
CC EMBL; AK010345; BAB26868.1; -
CC HSSP; Q99828; IDGV.
CC MGD; MGI:1344418; Cibi.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 2.
CC ProDom; PD000012; EF-hand; 1.

```

DR SMART: SM00054; EFH: 2.
 DR PROSITE: PS00018; EF-HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MM; C85B603A19P9D9AC CRC64;
 Query Match 94.5%; Score 904; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 6.4e-65;
 Matches 179; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 MGSGSRLSKELAEVODLFLTKOELLAHRRFCCLLPQEQRTVSSSLRAQVPEQIIS 60
 DB 1 MGSGSRLSKELAEVODLFLTKOELLAHRRFCCLLPQEQRTVSSSLRAQVPEQIIS 60
 OY 61 LPELKANPFRERICVFTSPAKQSLSFEDFDLLSVFSDTATPDIKSHAFRIFFDDDD 120
 DB 61 LPELKANPFRERICVFTSPAKQSLSFEDFDLLSVFSDTATPDIKSHAFRIFFDDDD 120
 OY 121 GTLNREXLSRLVNCITGEGEDRTLSSAEKQOLIDNILESDDIDROGTINLSEFOHYSRS 180
 DB 121 GTLNREXLSRLVNCITGEGEDRTLSSAEKQOLIDNILESDDIDROGTINLSEFOHYSRS 180
 OY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD: PRT; 191 AA.
 AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (CaMyrin) (DNA-PKcs
 DE Interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafield J., Stubli U., Bereliter-Hahn J., Strebhardt K., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: AF136585; AAF08368.1; -
 DR HSSP: Q99828; IDGV.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 DR ProDom: PD000012; EF-hand; 1.

DR SMART: SM00054; EFH: 2.
 DR PROSITE: PS00018; EF-HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MM; 3B00B0228879FC7 CRC64;
 Query Match 94.4%; Score 903; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 7.7e-65;
 Matches 179; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 MGSGSRLSKELAEVODLFLTKOELLAHRRFCCLLPQEQRTVSSSLRAQVPEQIIS 60
 DB 1 MGSGSRLSKELAEVODLFLTKOELLAHRRFCCLLPQEQRTVSSSLRAQVPEQIIS 60
 OY 61 LPELKANPFRERICVFTSPAKQSLSFEDFDLLSVFSDTATPDIKSHAFRIFFDDDD 120
 DB 61 LPELKANPFRERICVFTSPAKQSLSFEDFDLLSVFSDTATPDIKSHAFRIFFDDDD 120
 OY 121 GTLNREXLSRLVNCITGEGEDRTLSSAEKQOLIDNILESDDIDROGTINLSEFOHYSRS 180
 DB 121 GTLNREXLSRLVNCITGEGEDRTLSSAEKQOLIDNILESDDIDROGTINLSEFOHYSRS 180
 OY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD: PRT; 187 AA.
 AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain, and Testis;
 RX MEDLINE=99132027; PubMed=9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Horii T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Blochim. Biophys. Acta 1444:143-147(1999).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: AB016080; BAA36545.1; -
 DR HSSP: Q99828; IDGV.
 DR MGD: MGI:1929293; KIP2.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 3
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFH: 2.
 DR PROSITE: PS00018; EF-HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MM; D21D21DCB00B65FC CRC64;

[illegible]

DB 1 GAAPSKIYDGLLED-----TNDREIERLRKRFMKLRDSSGSSIDKN-----EFMSI 48
 QY 62 PELKANPFRKRICRVSTSPAKDSLSEFEDLLDLSVSTAPADIKSHAFRIEDDDG 121
 DB 49 PGVSSNPPLAGRIMEVFADNSGD-VDFOEFITGLSIFSGRSKDEKLRFAFYIDDKG 107
 QY 122 TLNREXLSRLVNCGLTEGEDRLSASEKMLDNLLESDIDRDGTINLSEFOHVI 177
 DB 108 FISNGELFIVIKIMVG-----SNLDEQQLQOIVDRTIVENDSGDGRLSSEERKNM 159
 RESULT 10
 CALB_HUMAN
 ID CALB_HUMAN STANDARD; PRT; 169 AA.
 AC P06705; P15117; Q08044;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
 GN PPP3R1 OR CNB OR CNA2.
 OS Homo sapiens (Human),
 OS Bos taurus (Bovine), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606, 9913, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RA Guertini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
 RT "Isolation and sequence of a cDNA clone for human calcineurin B, the
 RT Ca²⁺-binding subunit of the Ca²⁺/calmodulin-stimulated protein
 RT phosphatase";
 RL DNA 8:675-682(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RA Nardang C.E., Bottorff D.A., Adachi K.;
 RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-168.
 RC SPECIES-Bovine; TISSUE-Brain;
 RA MEDLINE=84132092; PubMed=6321184;
 RX Aitken A., Klee C.B., Cohen P.;
 RT "The structure of the B subunit of calcineurin";
 RL Eur. J. Biochem. 139:663-671(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
 RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES-Rat; TISSUE-Brain, and Testis;
 RX MEDLINE=94153993; PubMed=8110831;
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory
 RT subunit of Ca²⁺/calmodulin-dependent protein phosphatase (calcineurin
 RT B alpha 2).";
 RL Biochim. Biophys. Acta 1217:174-180(1994).
 RN [6]
 RP CALCIUM-BINDING DATA.
 RC SPECIES-Bovine;
 RX MEDLINE=80101597; PubMed=293720;
 RA Klee C.B., Crouch T.H., Krinks M.H.;
 RT "Calcineurin: a calcium- and calmodulin-binding protein of the
 RT nervous system";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RC SPECIES-Bovine;
 RX MEDLINE=93360994; PubMed=7543369;
 RA Griffith J.P., Kim J.L., Kim E.E., Shtechak M.D., Thomson J.A.,
 RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
 RT "X-ray structure of calcineurin inhibited by the immunophilin-
 RT 1 immunosuppressant FKBP12-FK506 complex";
 RL Cell 82:507-522(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES-Human;
 RX MEDLINE=96097077; PubMed=8524402;
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moosaw E.W.,
 RA Gastlino L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
 RA Bacquet R., Villafranca J.E.;
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-
 RT calcineurin complex";
 RL Nature 378:641-644(1995).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.
 CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
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 CC
 DR EMBL; M30773; AAB08721.1; -;
 DR EMBL; X71666; CAA50659.1; -;
 DR EMBL; L03554; AAA40854.1; -;
 DR EMBL; D14568; BAA03422.1; -;
 DR EMBL; D14425; BAA03318.1; -;
 DR PIR; A33391; A33391.
 DR PIR; S34127; S34127.
 DR PIR; JTO297; JTO297.
 DR PIR; S42716; S42716.
 DR PIR; S42717; S42717.
 DR PDB; 1A01; 03-DEC-97.
 DR PDB; 1TCO; 12-FEB-97.
 DR Genew; HGNC:9317; PPP3R1.
 DR MIM; 601302; -;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 4.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; Eph; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium-binding; Repeat; Alternative splicing; Myristate;
 KW 3D-structure.
 FT INIT_MET 0
 FT LIPID 1
 FT CA_BIND 30
 FT CA_BIND 41
 FT CA_BIND 62
 FT CA_BIND 73
 FT CA_BIND 99
 FT CA_BIND 110
 FT CA_BIND 140
 FT CA_BIND 151
 FT VARSPPLIC 1
 FT
 FT CONFLICT 11
 FT CONFLICT 153
 FT SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
 Query Match 19.4%; Score 185.5; DB 1; Length 169;
 Best Local Similarity 31.1%; Pred. No. 4e-08;

	Matches	38;	Conservative	32;	Mismatches	47;	Indels	5;	Gaps	2;
QY	56	EOILSLPELKANPKERICRVFSPAKDSLEDFDLVFSOTATPDIKSHYAFRIF	115							
		I: : : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : :								
Db	40	EEFMSLPELOQNPLVQRVIDIFDTD-CNGEVDKEFKEIEGVFSQSVKDEQKLRFAPIY	98							
		I: : : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : :								
QY	116	DFDDGGTLNREXLNCLTGEGEDTRLASASEMKQLDNIILEESDIDRDGTINLSEFOH	175							
		I: : : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : :								
Db	99	DMDKGGYISNGELFQVLKMMVG---NNLKDTQLQIVDKTTIINADKGDGGRISFEERCA	154							
		I: : : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : : I: : : :								
QY	176	VI	177							
		I: :								
Db	155	V	156							
		I: :								

```

RESULT 11
CALB_MOUSE
ID CALB_MOUSE STANDARD; PRT; 169 AA.
AC Q63810;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
DE 1).
DE PFP3R1 OR CNB.
GN PFP3R1 OR CNB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RN
RP
RC TISSUE=Brain;
RX MEDLINE=92392379; PubMed=1325794;
RA Ueki K., Muramatsu T., Kincaid R.L.;
RT "Structure and expression of two isoforms of the murine calmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).";
RL Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIM, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
-----
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CC      ENBL; S43864; AAB23171.1; -.
DR      HSSP; P06705; LAUL.
DR      MGD; MGI:107172; Ppp3rl.
DR      InterPro; IPR002048; EF-hand.
DR      Pfam; PF00036; ehand; 4.
DR      ProDom; PD000012; EF-hand; 2.
DR      SMART; SM00054; EFh; 4.
DR      SMART; PS00018; EF_HAND; 4.
DR      calcium-binding; Repeat; Myristate.
KW      INIT_MET 0 0
FT      LIPID 1 1
FT      CA_BIND 30 41
FT      CA_BIND 62 73
FT      CA_BIND 99 110
FT      CA_BIND 140 151
FT      SEQUENCE 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;
SQ

```

	Query Match	19.4%;	Score	185.5;	DB	1;	Length	169;
	Best Local Similarity	31.1%;	Pred.	No.	4e-08;			
	Matches	38;	Conservative	32;	Mismatches	47;	Indels	5;
	Gaps							
Qy	56	EQLSLPELKANPKERICRVFSTSPAKDSLSPEDFDLVSVFDSTATPDIKSHVAFRIF	115					
		: : : : : :	:	:	:	:	:	:
		: : : : : :	:	:	:	:	:	:
Dd	40	EEFMSLPQLQNVLVRVIDFTD-GNGEVDKFEIEGVQSFSVKDKRKLRFARIV	98					
		: : : : : :	:	:	:	:	:	:
		: : : : : :	:	:	:	:	:	:
Qy	116	DFDDGTLNREXLSRLVNCLTGEGEDTRLASSEMKLIDNILEESDTRDGTINLSEFOH	175					
		: : : : : :	:	:	:	:	:	:
		: : : : : :	:	:	:	:	:	:
Dd	99	DMKDGVYISNGELFQVLYKMVG---NNLKDTQLQIVDKTIINADKDGGRISPEEPCA	154					
		: : : : : :	:	:	:	:	:	:
		: : : : : :	:	:	:	:	:	:
Qy	176	VI	177					
		:	:					
Dd	155	VV	156					

RESULT 12.

ID	CALC_DROME	STANDARD;	PFT;	170 AA.
AC	Q24214; Q9V315;			
AD	01-NOV-1997 (Rel. 35, Created)			
AT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Calcineurin B subunit, isoform 2 (protein phosphatase 2B regulatory subunit).			
DN	CANB2 OR CNB2 OR CG11217.			
GN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Canton-S;			
RC	MEDLINE=97080515; PubMed=8921860;			
RX	Warren W.D., Phillips A.M., Howells A.J.;			
RA	"Drosophila melanogaster contains both X-linked and autosomal			
RT	homologues of the gene encoding calcineurin B.;"			
ET	Gene 177:149-153(1996).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkley;			
RC	MEDLINE=20196006; PubMed=10731132;			
RX	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.C., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers J., Blazer E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Wan K.H., Doyle C., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Abell J.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Ballew R.M., Basu A., Baxendale J., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Berson K.Y., Bencos P.V., Bouck J., Brockstein P., Brottlie P.,			
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottlie P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler A., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,			
RA	Palaolozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RL "The genome sequence of *Drosophila melanogaster*,"
Science 287:2185-2195(2000).
CC -!- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERES CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL: U56245; AAC47350.1; -
DR EMBL: AE003840; AAF59195.1; ALT_SEQ.
DR HSSP: P06705; ITCO.
DR Flybase: FBtr0015614; CanB2.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR PRODOM: PD000012; EF-hand; 2.
DR SMART: SM00054; Eph; 4.
DR PROSITE: PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA-BIND 31 42 EF_HAND 1 (POTENTIAL).
FT CA-BIND 63 74 EF_HAND 2 (POTENTIAL).
FT CA-BIND 100 111 EF_HAND 3 (POTENTIAL).
FT CA-BIND 141 152 EF_HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19267 MW; FDB1B9DB5A4BDEC CRC64;
Query Match 18.5%; Score 177.5; DB 1; Length 170;
Best Local Similarity 24.7%; Pred No. 1.7e-07;
Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;
OY 3 GSGSRSLKELLAEYDQFLFRLQELLHARRCELPQDRFVSSSLRAQVPEQLSLP 62
DB 2 GNETSLEPMEMCSNFD-----ADEIRRLGRF-----RKLDNDSGLSDVERMSDP 47
OY 63 ELKAMPFERICRVSTSPAKSLSEFEDLDLSFSDATPDICKHYAFRIFFDDSGT 122
DB 48 ELQNPPLVQRYVIDFD-ADNGEVEFKEPIQGVQSFVSKDKLSKLRFAFRIDMDNGY 106
OY 123 LNRXLSRLVNCITGEGEDTRLASEMKQLDNIIESSIDDDGTINLESEFOHIVRS 180
DB 107 ISNGELFVYKMGV-----NNLKDTQLOQIDVKTIGFADKDEGKISFDEFSYVGT 160
RESULT 13
CA22_MOUSE
ID CA22_MOUSE STANDARD; PRT: 194 AA.
AC 062877;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (calcineurin

DE homologous protein) (S1d470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd K.K., Devitt N.D., Chang A., Mills K.,
RA Szul E.S.;
RT "A novel Ca2+-binding protein, p22, is required for constitutive
RT membrane traffic";
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsunoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.;
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na+/H+
RT exchanger";
RN J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata J., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.
CC -!- PTM: BOTH N-METHYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL: U39875; AA004146.1; -
DR EMBL: AB070350; BAB63369.1; -
DR EMBL: AB025217; BAA84688.1; -

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DR EMBL; AK005067; BAB23791.1; -.
DR HSSP; P06705; IAU1.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INT_MET 0
FT LIPID 1
FT DOMAIN 38
FT DOMAIN 70
FT CA_BIND 122
FT CA_BIND 163
FT MUTAGEN 133
FT SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 18.5%; Score 177; DB 1; Length 194;
Best Local Similarity 26.8%; Pred. No. 2.2e-07;
Matches 52; Conservative 35; Mismatches 75; Indels 32; Gaps 6;

QY 5 GSR-----LSKELLAEYODLFTLQKTEILLAHRRFCELLPOQRVVESSLRAQVPEQILS 60
DB 1 GSRATLRLDELEIEIKETGFSQITRLYSRFTSLDKGNGFLSR-----t-----EDFOR 52
QY 61 LPKLKPNFKERICRVFTSPAKDSLSFEDFLDLLSVF-----SDTATPD----- 105
DB 53 IPELAINPLGLRIINAF-FSEGDQVNFGRFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111
QY 106 IKSHYARIFDDDDGILNREXLSRLNCLTGEGEDTRLGSASEMKQLINDLESIDTRD 165
DB 112 NKLHFAFLYDLDDKISRDELQVLRLMVGV-----VNISDEQLGSLADRTIQEADQDGD 167
QY 166 GTINLSEFOHVISR 179
DB 168 SAISFTFEFVKVLEK 181

RESULT 14
CALB_DROME STANDARD; PRT; 170 AA.
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory
DE subunit).
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=13311060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two
RT subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RA Adams M.D., Cealnikar S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers J.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- PROTEIN: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC FUNCTION FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; M97215; AAA28411.1; -.
CC EMBL; AE003434; AAP46026.1; -.
CC HSSP; P06705; ITCO
CC FlyBase; FBgn0010014; CanB.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31
FT CA_BIND 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
FT SEQUENCE 170 AA; 19341 MW; 77D89BE9D961900 CRC64;

Query Match 18.1%; Score 173.5; DB 1; Length 170;
Best Local Similarity 26.5%; Pred. No. 3.6e-07;
Matches 41; Conservative 38; Mismatches 63; Indels 13; Gaps 3;

QY 26 EILLAHRRFCELLPOQRVVESSLRAQVPEQILSLPELKANPKERICRVFTSPAKDS 85
DB 19 EIRLGRFR-----RKLDLNSGALSIDFMSLPELQONPLVQRVIDIFD-ADNGNE 69

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QY 86 LSFEDFDLVSFSDTATPDIKSHYAFRIEFDGDTLNREXLSRLVNCITGEGEDTRLIS 145
 Db 70 VDFEFIOGVQSOFVSFRDCKLSKLRFAFRIVYDMNDGYISNELQVLMWVG---NNLK 125
 QY 146 ASEMKOLINDILESDDIDROGTLINLSEFOHYISRS 180
 Db 126 DTQLQOTVDKTIKCPADKDEGKISDFECISVWNT 160

RESULT 15
 CA22.HUMAN
 ID CA22.HUMAN STANDARD; PRT; 194 AA.
 AC 099653;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin
 homologous protein) (Calcineurin B homolog).
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X., Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H
 exchange".
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RM [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY
 SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE
 SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A
 DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE
 ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed. HAS BEEN FOUND IN
 FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
 CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC
 (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS
 ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE
 PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

CC -----
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 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; U61538; AAB37770.1;
 DR EMBL; BC001646; AAH01646.1;
 DR HSSP; P06705; IAU1.
 DR MIM; 606988;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR PRODOM; PD000012; EF-hand; 2.
 DR SMART; SM00054; Efn; 2.
 DR PROSITE; PS00018; EF_HAND; FALSE NEG.
 DR Calcium-binding; Repeat; Myristate; Phosphorylation.
 KM INIT_MET 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT DOMAIN

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SO SEQUENCE 194 AA; 22325 MM; 17DDE5F03C8380 CRC64;

Query Match 18.0%; Score 172; DB 1; Length 194;
 Best Local Similarity 26.3%; Pred. No. 5.6e-07;
 Matches 51; Conservative 35; Mismatches 76; Indels 32; Gaps 6;

QY 5 GSR-----LSKELLAEYODLTFELKOEILLARFPCELLPOQRTVSSILRAQVFEGLIS 60
 Db 1 GSRATLLRDELEIKETGFSHQITRLXSRFTSLDKGNGITLSR-----EDFQR 52

QY 61 LPEIKANPEKRIQVSTSPAKDSLSEFEDLILSVF-----SDTATPD----- 105
 Db 53 IPELAINPLGDRITNAFPE-GEQVNRGEMRTLAHRPTEDNEKSGDVNGPPLNSRS 111

QY 106 IKSHYAFRIEFDGDTLNREXLSRLVNCITGEGEDTRLISASEMKOLINDILESDDIRD 165
 Db 112 NKLHFAFRLYDLDEKISRDELQVLMWVG---VNISDEQGLSIADRTIGPADODGD 167

QY 166 GTINLSEFOHYISR 179
 Db 168 SAISFTFEVYLER 181

Search completed: January 17, 2003, 12:48:33
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:03 : Search time 35 seconds
(without alignments)
727.168 Million cell updates/sec

Title: MUT127
Sequence: 1 MCGSGSRSLKELAEYQDLT.....EFQHVIRSPDFASSFKIVL 191
Perfect score: 957

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_101002:*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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- 9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	99.4	191	19	AAW51215
2	945	98.7	191	19	AAW62287
3	943	98.5	191	19	AAW64199
4	372	38.9	172	22	AAU87324
5	372	38.9	184	22	AAW43562
6	370	38.7	185	22	AAW64418
7	355	37.1	173	22	ABB96054
8	355	37.1	173	22	AAU87612
9	355	37.1	173	22	AAW95362
10	355	37.1	173	22	AAW43637

11	355	37.1	173	22	AAU19952
12	338	35.3	187	22	AAE09736
13	337.5	35.3	206	22	ABB64325
14	237.5	24.8	169	23	ABP41194
15	220	23.0	120	20	AAV11976
16	201.5	21.1	175	20	AAV00881
17	188	19.6	175	21	AAAG21178
18	188	19.6	210	21	AAAG21177
19	187	19.5	175	21	AAAG51586
20	187	19.5	175	23	ABB92357
21	185	19.3	175	21	AAAG07824
22	183.5	19.2	170	19	AAW64200
23	183.5	19.2	170	21	AAW09788
24	179.5	18.8	189	22	AAW65936
25	178	18.6	169	21	AAAG51587
26	176	18.4	169	21	AAAG07825
27	174	18.2	169	21	AAAG21179
28	173.5	18.1	187	22	ABB61857
29	173.5	18.1	187	22	ABB67063
30	172.5	18.0	162	22	ABB65554
31	171.5	17.9	170	22	ABB60493
32	167	17.5	170	21	AAW09977
33	167	17.5	170	22	AAO14411
34	167	17.5	173	22	AAW64410
35	167	17.5	187	22	AAW07327
36	167	17.5	189	22	AAW95936
37	167	17.5	189	22	AAW87615
38	167	17.5	189	22	AAW95239
39	167	17.5	189	22	AAW43564
40	167	17.5	189	22	AAW43639
41	167	17.5	189	22	AAW47032
42	161.5	16.9	226	21	AAAG47032
43	160.5	16.8	226	21	AAAG21763
44	154	16.1	190	21	AAW69996
45	153	16.0	194	22	AAW07385

ALIGNMENTS

RESULT 1	
AAW51215	AAW51215 standard; Protein; 191 AA.
ID	AAW51215
XX	
AC	AAW51215;
XX	
DT	21-AUG-1998 (first entry)
XX	
DE	Amino acid sequence of the calcium-integrin binding protein.
XX	
KW	Human calcium-integrin binding protein; CIB; integrin alpha IIB;
KM	Cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor
XX	Inhibition; blood coagulation; vascular disorder.
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	116..128
FT	/note="EF-hand motif"
FT	160..173
FT	/note="EF-hand motif"
XX	
PN	WO9814471-A1.
XX	
PD	09-APR-1998.
XX	
XX	24-SEP-1997; 97MO-US16828.
PF	
XX	
XX	02-OCT-1996; 96US-0720625.
PR	
XX	
PA	(UYN-C) UNIV NORTH CAROLINA.
XX	
PI	Naik UP, Parise LV;

Novel human calciu
Human Kinase Inter
Drosophila melanog
Human ovarian anti
Human 5' EST seque
Calcineurin regula
Zea mays protein f
Arabidopsis thalia
Herbicideally activ
Arabidopsis thalia
Human HCNB protein
Human HCNB protein
Drosophila melanog
Arabidopsis thalia
Zea mays protein f
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human CNBT protel
Calcineurin B subu
Amino acid sequenc
Novel central nerv
Human testicular a
Novel central nerv
Human reproductive
Human polypeptide
Human polypeptide
Novel human calciu
Arabidopsis thalia
Arabidopsis thalia
Human receptor-ass
Novel central nerv

XX WPI: 1998-240018/21.
DR N-PSDB; AAV07211.
XX New isolated calcium-integrin binding protein - is expressed in
PT platelets and activates the fibrinogen receptor, used to develop
PT products for treating e.g. vascular disorders
XX
PS Claim 1; Page 30; 44pp; English.
XX This is the amino acid sequence of the human calcium-integrin binding
CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
GC domain. The CIB protein is expressed in platelets and interacts with
CC the alpha IIB subunit of integrin alpha IIB-beta 3, to activate the
CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
CC activation of the fibrinogen receptor where it is desired to reduce
CC blood coagulation for therapeutic, diagnostic or pharmaceutical
CC reasons. The products can be used for treating vascular disorders,
CC and for isolating or purifying integrins or fibrinogen. They can also
CC be used for detection and diagnosis.
XX
XX Sequence 191 AA;
Query Match 99.4%; Score 951; DB 19; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.9e-95;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGGSGRLSKELLAQYQDLTFLTKQELLAHRRFCCELLPQEQRTVESLRAQVPEQILS 60
DB 1 MGGSGRLSKELLAQYQDLTFLTKQELLAHRRFCCELLPQEQRSVSSLRAQVPEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEDFDD 120
DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEDFDD 120
QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
DB 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSEFKIVL 191
DB 181 PDFASSEFKIVL 191
RESULT 2
AAW62287
XX ID AAW62287 standard; Protein: 191 AA.
XX AC AAW62287;
XX 24-SEP-1998 (first entry)
XX Human protein phosphatase regulatory subunit.
XX Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
KW immunosuppression; neurodegeneration; inflammation; cancer.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 44 /label= unknown
FT /note= "encoded by ASG"
FT Misc-difference 45 /label= unknown
FT /note= "encoded by TGN"
XX W09826056-A1.
XX 18-JUN-1998.
XX 25-NOV-1997; 97WO-US21603.
XX

PR 12-DEC-1996; 96US-0764563.
XX (INCY-) INCYTE PHARM INC.
XX Goli SK, Hillman JL;
XX WPI: 1998-348518/30.
DR N-PSDB; V398009.
XX
XX New protein phosphatase regulatory sub-unit - useful for diagnosis,
PT prevention and treatment of immuno-suppression, neuro-degeneration,
PT inflammation and cancer
XX
XX Claim 1; Fig 1; 65pp; English.
XX The present sequence is a pure human protein phosphatase regulatory
CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
CC HCNB, are used to produce recombinant HCNB which is used to treat or
CC prevent immunosuppression or neurological diseases (especially parasitic,
CC bacterial or viral infections, including AIDS; the effects of radio- or
CC chemo-therapy and Alzheimer's disease). Antagonists which bind
CC specifically to HCNB and modulate its activity are used to treat
CC inflammation, cancer, or immunological disorders and allograft rejection
CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
CC arthritis). Complements of the DNA encoding HCNB are useful as probes
CC and primers for detecting the DNA encoding HCNB by hybridisation or
CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
CC particularly for diagnosis of the specified disorders, including early
CC diagnosis of cancers. The probes can also be used to map the
CC corresponding genomic sequence, while Ab are also useful in drug
CC screening and for purifying native HCNB. Therapeutic agents are
CC administered orally, intravenously, intramuscularly, topically or
CC rectally, normally at 0.1-105 mu g.
XX
XX Sequence 191 AA;
Query Match 98.7%; Score 945; DB 19; Length 191;
Best Local Similarity 98.4%; Pred. No. 1.3e-94;
Matches 188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGGSGRLSKELLAQYQDLTFLTKQELLAHRRFCCELLPQEQRTVESLRAQVPEQILS 60
DB 1 MGGSGRLSKELLAQYQDLTFLTKQELLAHRRFCCELLPQEQRXESSLRAQVPEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEDFDD 120
DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEDFDD 120
QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
DB 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSEFKIVL 191
DB 181 PDFASSEFKIVL 191
RESULT 3
AAW64199
XX ID AAW64199 standard; Protein: 191 AA.
XX AC AAW64199;
XX 09-NOV-1998 (first entry)
XX Human interferon receptor 1 binding protein IrlB1.
XX Interferon receptor 1 binding protein; IrlB1; human; tumour;
KW cancer; gene therapy; tissue graft; graft survival.
XX Homo sapiens.
XX

PR	14-SEP-2000;	2000US-02323397.
PR	14-SEP-2000;	2000US-02323398.
PR	14-SEP-2000;	2000US-02323399.
PR	14-SEP-2000;	2000US-02323400.
PR	14-SEP-2000;	2000US-02323401.
PR	14-SEP-2000;	2000US-02323063.
PR	14-SEP-2000;	2000US-02323064.
PR	14-SEP-2000;	2000US-02323065.
PR	21-SEP-2000;	2000US-0234223.
PR	21-SEP-2000;	2000US-0234274.
PR	25-SEP-2000;	2000US-0234997.
PR	25-SEP-2000;	2000US-0234998.
PR	26-SEP-2000;	2000US-0234984.
PR	27-SEP-2000;	2000US-0235834.
PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	02-OCT-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	02-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241221.
PR	20-OCT-2000;	2000US-0241785.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
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PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249219.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.

PR	05-DEC-2000;	2000US-0751030.
PR	05-DEC-2000;	2000US-0351988.
PR	05-DEC-2000;	2000US-0267119.
PR	06-DEC-2000;	2000US-0251479.
PR	06-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC	

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-581633/65.

N-PSDB: ABK43654.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 9: SEO ID No 842: 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 38.98; Score 372; DB 22; Length 172;

Query Match	Best Local Similarity	Pred. No.	2.7e-32;
30.5%	43.58%		

Best Local Similarity	45.56; 11.89		
Matches	77;	Conservative	36; Mismatches
			54; Indels
			10; Gaps

13 IAEYODITETITKOEITIAHRRFCELLPOEORTVESSLRAQVPFEQILSLPELKANPFKER 72

QY I3 LAEI QDU LIF LI KQEI TPDHAKK CEEEF QEQA V DDDHHG V V EEE

1 LEEYOALFTLRNEILCIHDTFLKLCPPGKYKEATL-----TMDQVSSLPALRVNPFDR 56

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QV 73 ICRVFSTSPAKDLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDGTLNREXLSRLV

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RESULT 5

RESOL 2
AAM43562

ID	AAM43562 standard; Protein; 184 AA.
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AC AAM43562;

XX
DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 240.
DE
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiangiogenic; hepatotropic; antidiabetic;
KW antiinflammatory; antilucer; vulnery; anticovulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX WO200155308-A2.
XX
PD 02-AUG-2001.
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PE 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217486.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

05-DEC-2000; 2000US-0256719.
 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251868.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-488781/53.
 N-PSDB; AAI63868.
 New isolated nucleic acids and polypeptides, useful for diagnosing,
 treating and/or preventing human diseases and disorders -
 Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
 The invention relates to human polynucleotides (AAI63803-AAI64012) and
 the encoded proteins (AAM43497-AAW43660) useful for preventing, treating
 or ameliorating medical conditions e.g. by protein or gene therapy. The
 genes were isolated from a range of human tissues disclosed in the
 specification. The nucleic acids, proteins, antibodies and (ant)agonists
 are useful in the diagnosis, treatment and prevention of: (a) cancer,
 e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Query Match 38.9%; Score 372; DB 22; Length 184;
 Best Local Similarity 43.5%; Pred. No. 2.9e-32;
 Matches 77; Conservative 36; Mismatches 54; Indels 10; Gaps 3;
 13 LAEYQDTFTLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLPELKANPFKE 72
 13 LEEYQALTFTLRNEILCIHTDFLKLCPGKYKEATL---TMDQVSSLPALRVNPFDR 68
 73 ICRVFSTSPAKDSLSFEDFLDLSVFSPTATPDIKSHYAFRIEFDGDTLNREXLSLV 132
 69 ICRVFS---HKGMFSEFVGLGMAVSFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 125
 133 NCLTGEGETRLSASEMKQLIDNILESDIDRGTINLSFQHVIRSPDFASFSFKI 189
 126 LRLNSDD---MSEDLMDLTNHLVSESDLDNDNMLSFSEFEHAKSPDFMNSPRI 179
 RESULT 6
 AAB64418
 ID AAB64418 standard; Protein; 185 AA.
 AC AAB64418;
 22-MAR-2001 (first entry)
 Amino acid sequence of human intracellular signalling molecule INTRA50.
 Human; intracellular signalling molecule; INTRA; immunosuppressive;
 cytoskeletal; neuroprotective; neurotropic; antiarteriosclerotic; cancer;
 antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
 KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
 KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
 KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
 KW mental disorder; schizophrenia; anxiety.
 XX Homo sapiens.
 OS WO200077040-A2.
 PN 21-DEC-2000.
 XX 16-JUN-2000; 2000WO-US16636.
 XX 16-JUN-1999; 99US-0139566.
 PR 17-AUG-1999; 99US-0149640.
 PR 09-NOV-1999; 99US-0164417.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
 PI Azimzai Y, Yang J, Reddy R, Lu DAN;
 PI N-PSDB; AAF32687.
 XX WPI; 2001-025334/03.
 DR New human intracellular signalling molecules, useful for the diagnosis,
 XX prevention and treatment of cell proliferative, autoimmune,
 PT inflammatory, neurological, gastrointestinal, reproductive and
 PT developmental disorders -
 PT Claim 5; Page 158-159; 192pp; English.
 PS Sequences AAF32638 - AAF32689 represent cDNA encoding human
 CC intracellular signalling molecules INTRA1 - INTRA52, represented in
 CC AAB4309 - AAB64420. Modulators of the intracellular signalling molecules
 CC of the invention exhibit immunosuppressive, cytostatic; neuroprotective;
 CC neurotropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
 CC antihelminthic; antibacterial; antifungal; antiviral; antiparasitic;
 CC agonists and antagonists are useful for the treatment of a condition
 CC associated with decreased or increased expression of functional INTRA.
 CC Disorders associated with abnormal INTRA expression or activity include
 CC cell proliferative disorders e.g. arteriosclerosis and cancers;
 CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
 CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
 CC protozoal and helminthic infections; gastrointestinal disorders e.g.
 CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
 CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jacob
 CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
 CC disorder. Antibodies immuno specific for the INTRA proteins may also be
 CC useful in the diagnosis of the above disorders.
 SQ Sequence 185 AA;
 Query Match 38.7%; Score 370; DB 22; Length 185;
 Best Local Similarity 43.6%; Pred. No. 4.9e-32;
 Matches 78; Conservative 35; Mismatches 56; Indels 10; Gaps 3;
 QY 11 ELAEYQDTFTLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLPELKANPFK 70
 DB 12 EDLEEQALTFTLRNEILCIHTDFLKLCPGKYKEATL---TMDQVSSLPALRVNPF 67
 QY 71 ERICRVFSTSPAKDSLSFEDFLDLSVFSPTATPDIKSHYAFRIEFDGDTLNREXLSR 130
 DB 68 DRIICRVFS---HKGMFSEFVGLGMAVSFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQ 124
 QY 131 LVNCLTGEGETRLSASEMKQLIDNILESDIDRGTINLSFQHVIRSPDFASFSFKI 189
 DB 125 IILRLNSDD---MSEDLMDLTNHLVSESDLDNDNMLSFSEFEHAKSPDFMNSPRI 180
 RESULT 7

AB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
OS Homo sapiens.
XX
PN W0200155317-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01329.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483232/52.
XX XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
PT useful for preventing, diagnosing and/or treating testicular cancer
PT
XX
XX Claim 11; SEQ ID NO 1438; 766pp; English.
XX
XX The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a protein of the
CC invention.
XX
XX Sequence 173 AA;
SQ
Query Match 37.18; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;
QY 13 LAEYQDLFLKQETLLAHRRFCELLPQETVSSLRAPVFEQILSLPELKANPKFER 72
DB 1 LEEYQALFLTRNEILCHIDFLKCPGKYKEATL----TMDQVSSLPALRVNPFDR 56
QY 73 ICRVFTSPAKDSLFEDFLDLSVSTATPDIKSHVAFRIFDDGDTLNREXLSRLV 132
DB 57 ICRVFS---HKGMFSEFVLGNASVFEQACPSLKIEYAFRIYDENGFIDEEDLQRII 113
QY 133 NCLTGEGETRLSASEMKQLINDILEESDIDEDGTINLSEQHVIHSRSPDEASSF 187
DB 114 LRLNSDD---MSEDLLMDLTNHLVLSXDLNDNMLSFSEFEHAMAKSPDFMTPF 165
RESULT 8
AAU87612
ID AAU87612 standard; Protein; 173 AA.
XX
AC AAU87612;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #52.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.

XX WO200155318-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01332.
XX
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
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PR 21-SEP-2000; 2000US-0234223.
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PR 25-SEP-2000; 2000US-0234998.
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PR 27-SEP-2000; 2000US-0235834.

XX
PA (HUMA -) HUMAN GENOME SCI INC.
XX

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (II) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated included autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysgenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired Immunodeficiency Virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, to

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0Y 13 LAEQDITFLTKOELLNHRFCCELLPQEQRTVESSRAQVPEEQITSLPELKNPFKER 72
      | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
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0Y 13 ICRFSTBPAKDSLSFEDFDLLSVFSODTAPPDIKSIYAFRFDQDDGTLNEXLSKV 132
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57 13 ICRVFS---HKGMFSFEDVLGMASYFSEQACPSLKIEYAFRIYDFENENGFIDEEDLQRTI 113

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QY 133 NCLTGEGETRLSASEMKOJDNIEESDIDRDGTJNLSEFOHVITSSPDPFASSE 187
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db 114 LRLNSDD--MSDDLMDLTNHVLSXSDLDNDNMJTSFSEFEHAMAKSPDFETPFE 165
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RESULT 9
AAM95362
ID AAM95362 standard; Protein; 173 AA.

DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
VY

KW Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.

05 Homo sapiens.

PN W0200155320-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01339.

PR 31-JAN-2000; 2000US-0179065.
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 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PR Rosen CA, Barash SC, Ruben SM;
 PR WPI: 2001-465570/50.
 PR N-PSDB; AAL01332.
 PR Isolated nucleic acid molecule encoding a reproductive system antigen
 PR is used in preventing, treating or ameliorating a medical condition

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XX Claim 11: SEQ ID NO 4020; 1297bp + Sequence Listing; English.
PS
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 173 AA;

Query Match 37.1%; Score 355; DB 22: Length 173;
Best Local Similarity 42.3%; Pseq No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

QY 13 LAEYODLFTLKQKILLAHRRFCELLPOEQRVSESLRAQVFEQILSLPELKNPFKR 72
Db 1 LEEYQALFTLRNELLCHDFELKCPGKYYKENTL---TMOVSSLPALRVAFEDR 56

QY 73 ICRVFTSPADSLSEFEDLLSVFSDTATPDIKSHAFNIFDDGTLNREXLSRLV 132
Db 57 ICRVFS---HKGMFSFEDVLGMASVFSEACPSLKTEYAFRIYDENNGFIDEEDLQRTI 113

QY 133 NCLTGEEDTRLASAEKMLIDNILESDIDRDGTINISEQHVYSRSPDASSF 187
Db 114 LRLNSDD---MSFDLMDLTNHYLSXSDLDNMKLSFEFEHMAKSPDEWTPF 165

RESULT 10
AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX
AC AAM43637;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide; SEQ ID NO 315.
XX
KW Human; antiarthritic; antiinflammatory; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virocidic;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiarrhythmic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
KW antiparasitic; cardiatic; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
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PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0232080.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
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PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236337.
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PR 29-SEP-2000; 2000US-0236337.
PR 29-SEP-2000; 2000US-0236338.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246523.
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 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-488781/53.

DR N-PSDB; AA163943.

XX New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -

XX Claim 11; SEQ ID NO 315; 664pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAW43449-AAW43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 173 AA;

XX Query Match 37.1%; Score 355; DB 22; Length 173;

XX Best Local Similarity 42.3%; Pred. No. 1.9e-30;

XX Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

OY 13 LAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSLRQVPEQILSLPELKANPKER 72

DB 1 LEEYQALTEFLTRNEILCIHDTFLKLCPPGKYKEATL---TMDQVSSLPALRVNPPDR 56

OY 73 ICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEDDDGTLNREXLSRLV 132

DB 57 ICRVFS---HKGWFSFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGIDEDLQRII 113

OY 133 NCLTGEGETRLSASEMKOLIDNILEESDIDRDGTINLSEFQHVISRPDFASSF 187

DB 114 LRLNSDD---MSEDLMLDLTNNHVLXSXDLNDNMLSFSEFEHAMAKSPDFMTTPF 165

RESULT 11

AAU19952

ID AAU19952 standard; Protein; 173 AA.

XX AC AAU19952;

XX DT 06-DEC-2001 (first entry)

XX DE Novel human calcium-binding protein #61.

XX KW Human; calcium-binding protein; calcium flux; neurological disease;

XX KW Immune dysfunction; digestive disorder; neoplastic disease;

XX KW Blood disorder; infectious disease; gene therapy; immunosuppressive;

XX KW Antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;

XX KW Virucide.

OS Homo sapiens.

XX WO200155304-A2.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01302.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

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PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

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PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

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PR 13-OCT-2000; 2000US-0239335.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(XHMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465568/50.
N-PDSB; AAS31637.

PT Isolated nucleic acid molecule encoding a calcium-binding protein is
used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID No 149; 542pp; English.

CC The present invention relates to the isolation of novel human
CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC novel calcium-binding proteins are also useful as screening tools to
CC identify antagonists and/or agonists that may enhance or inhibit
CC activities mediated by calcium-binding proteins. The polynucleotides of
CC the invention are also useful in gene therapy. AAU19892-AAU19969
CC represent the novel human calcium-binding proteins.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 173 AA:
Query Match 37.1%; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1,9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

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 DB 1 LEEYQALFLTRNEITLCHDTFLKCPGKYKEATL-----TMDQVSSLPALRYNPPRDR 56
 QY 73 ICRVSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDODGTNLNREKLSRLV 132
 DB 57 ICRVFS---HGKMSFEDVLGMSVFSQACPSLKIEYAFRIYDFENGFIDEEDLQRII 113
 QY 133 NCLTGEEDTRLASSEMQLDNLIEESDIDRDGTINLSEPHQVISPDPASSF 187
 DB 114 LRLNSDD---MSEDLMLDNLNHLVLSXSDLDNMLSPSEFAHAMAKSPDWTFF 165
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 ID AAE09736 standard; Protein: 187 AA.
 AC AAE09736;
 DT 29-NOV-2001 (first entry)
 DE Human kinase interacting protein.
 KW Human; kinase interacting protein; novel human protein; NHP;
 KW gene therapy; drug screening; mental disorder; biological disorder;
 KW medical disease; nontropic.
 XX Homo sapiens.
 OS WO200166760-A2.
 PN 13-SEP-2001.
 PD 08-MAR-2001; 2001WO-US07499.
 PF 08-MAR-2000; 2000US-0187719.
 PR (LEXI-) LEXICON GENETICS INC.
 PA Mathur B, Turner CA;
 PI WPI: 2001-557870/62.
 DR N-PSDB; AAD16796.
 XX Novel polynucleotides encoding human kinase interacting protein useful
 PT for drug screening, diagnosis and in gene therapy of biological
 PT disorders
 PS Claim 2; Page 31-32; 32pp; English.
 CC The present amino acid sequence is a novel human protein (NHP),
 CC human kinase interacting protein. NHP oligonucleotides are useful
 CC as hybridisation probes for screening libraries and assessing gene
 CC expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene are used to design primers for
 CC use in amplification assays to detect mutations within the exons,
 CC splice sites, introns that can be used in diagnostics and
 CC pharmacogenomics. NHP nucleotide sequences are useful for drug
 CC screening and nucleotide construct encoding NHP products are
 CC useful in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo.
 CC The encoded NHP polypeptides are useful for generating antibodies,
 CC as reagents in diagnostic assays, for identifying other cellular
 CC gene products related to NHP and as reagents in assays for screening
 CC for compounds that are useful in the treatment of mental, biological
 CC or medical disorders and diseases.
 XX Sequence 187 AA;
 SQ Query Match 35.3%; Score 338; DB 22; Length 187;
 Best Local Similarity 39.9%; Pred. No. 1.5e-28;
 Matches 77; Conservative 42; Mismatches 62; Indels 12; Gaps 5;

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 DB 1 MGNQOTVTFHQLEAYQDCTFTTKREIMRLRYQDLAPQLVPLDYTTCPD---VKVPE 57
 QY 57 QILSLPELKANPKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIED 116
 DB 58 LIGSMPELKDNPFRRQIAQVES-EDGDGHMTLDNFDLDMFSYNSMAPRDLKAYAFKIYD 116
 QY 117 FDDGTNLNREKLSRLVNCITGEGEDTRLASSEMQLDNLIEESDIDRDGTINLSEPHQV 176
 DB 117 FNNDYICAWDELTQVTYTKLT-RGE---LSAEVSLVCKVLDEADGDHGRSLSEDFQNM 172
 QY 177 ISRSPDFASSEFKI 189
 DB 173 ILRAPDFLSTFHI 185
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 AC ABB64325;
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 19787.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmacological.
 KW Drosophila melanogaster.
 OS WO200171042-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI: 2001-656860/75.
 DR N-PSDB; ABL08428.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure; SEQ ID NO 19787; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16175-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 206 AA;
 SQ Query Match 35.3%; Score 337.5; DB 22; Length 206;
 Best Local Similarity 43.8%; Pred. No. 2e-28;
 Matches 77; Conservative 31; Mismatches 51; Indels 17; Gaps 5;

QY 17 QDLTFLTKQETLLAHRRCCELLPO---EORTVESSLRAQVFPFQILSLPELKANPKERI 73

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23.0%; Score 220; DB 20; Length 120;

1 MCGSGRLSKELLA EYQDLTFLTKQEILLAHRRFCELLPQEQTVESSLRAQVPFEQILS 60

61 LPELKANP 68

61 FQSSRPTP 68

Search completed: January 17, 2003, 12:43:08


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; Sequence 2, Application US/09878454A
; GENERAL INFORMATION:
; APPLICANT: Monteliro, et al.
; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
; FILE REFERENCE: 4115-161
; CURRENT APPLICATION NUMBER: US/09/878,454A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,939
; PRIOR FILING DATE: 2000-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2:
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; ORGANISM: Homo sapiens
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ysm127
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Perfect score: 957

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1: /cgn2-6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2-6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2-6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2-6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2-6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2-6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	953	99.6	191	4	US-08-720-625-2
2	928	97.0	191	3	US-08-764-563-1
3	215.5	22.5	177	3	US-08-764-563-3
4	203.5	21.3	174	1	US-08-328-322-17
5	192.5	20.1	157	1	US-08-328-322-15
6	185.5	19.4	169	4	US-08-720-625-4
7	185.5	19.4	170	3	US-08-764-563-5
8	175	18.3	186	3	US-08-655-352-8
9	175	18.3	186	4	US-09-258-016-8
10	175	18.3	186	4	US-09-257-825B-8
11	171.5	17.9	186	4	US-09-258-016-8
12	152.5	15.9	196	3	US-08-764-563-4
13	149	15.6	193	3	US-09-048-889-1
14	149	15.6	193	3	US-08-655-352-3
15	149	15.6	193	4	US-09-258-016-3
16	142	14.8	220	4	US-09-257-825B-3
17	142	14.8	220	4	US-09-399-913-26
18	141	14.7	191	3	US-08-298-731-26
19	141	14.7	191	4	US-08-655-352-7
20	141	14.7	191	4	US-09-258-016-7
21	138	14.4	193	4	US-09-257-825B-7
22	138	14.4	193	3	US-08-655-352-2
23	137	14.3	193	4	US-09-258-016-2
24	137	14.3	216	4	US-09-389-913-6
25	137	14.3	216	4	US-09-298-731-6
26	137	14.3	250	4	US-09-399-913-24
27	137	14.3	220	4	US-09-298-731-24

28	137	14.3	227	4	US-09-399-913-8	Sequence 8, Appl1
29	137	14.3	227	4	US-09-399-913-10	Sequence 10, Appl1
30	137	14.3	227	4	US-09-298-731-8	Sequence 8, Appl1
31	137	14.3	227	4	US-09-298-731-10	Sequence 10, Appl1
32	137	14.3	245	4	US-09-399-913-4	Sequence 4, Appl1
33	137	14.3	245	4	US-09-298-731-4	Sequence 4, Appl1
34	137	14.3	252	4	US-09-399-913-20	Sequence 20, Appl1
35	137	14.3	252	4	US-09-298-731-20	Sequence 20, Appl1
36	137	14.3	270	4	US-09-399-913-14	Sequence 14, Appl1
37	137	14.3	270	4	US-09-298-731-14	Sequence 14, Appl1
38	136	14.2	216	4	US-09-399-913-2	Sequence 2, Appl1
39	136	14.2	216	4	US-09-298-731-2	Sequence 2, Appl1
40	134	14.0	270	4	US-09-399-913-18	Sequence 18, Appl1
41	134	14.0	270	4	US-09-298-731-18	Sequence 18, Appl1
42	133	13.9	193	3	US-08-655-352-4	Sequence 4, Appl1
43	133	13.9	193	4	US-09-258-016-4	Sequence 4, Appl1
44	133	13.9	193	4	US-09-257-825B-4	Sequence 4, Appl1
45	132	13.8	191	3	US-08-655-352-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Nalk, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2
Query Match
Best Local Similarity 99.6% Score 953; DB 4; Length 191;
Matches 189; Conservative 2; Mismatches 0; Indels 0; Gaps 0
OY 1 MGSSGSRSLKELAEYQDLTFLTKKEILLARRPCELLPOQRVYESSLRQAVPEQILS 60
DB 1 MGSSGSRSLKELAEYQDLTFLTKKEILLARRPCELLPOQRVYESSLRQAVPEQILS 60
OY 61 LPELKNFRRICRVESTSPAKDLSFEDFLDLIVSPDPTDISHVAFRIFDDDD

Db 61 LPEKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDGDD 120
 QY 121 GTLNREXLSRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVIRS 180
 Db 121 GTLNREXLSRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVIRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 2
 US-08-764-563-1
 ; Sequence 1, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,563
 FILING DATE: Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0178 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 191 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: Consensus

US-08-764-563-1
 Query Match 97.0%; Score 928; DB 3; Length 191;
 Best Local Similarity 98.4%; Pred. No. 3.3e-93;
 Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEYQDLTTLTKQEIILAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60
 Db 1 MGGSGSRLSKELLAEYQDLTTLTKQEIILAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60
 QY 61 LPEKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDGDD 120
 Db 61 LPEKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDGDD 120
 QY 121 GTLNREXLSRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVIRS 180
 Db 121 GTLNREXLSRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVIRS 180

QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 3
 US-08-764-563-3
 ; Sequence 3, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,563
 FILING DATE: Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0178 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 177 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 458230
 US-08-764-563-3

Query Match 22.5%; Score 215.5; DB 3; Length 177;
 Best Local Similarity 29.2%; Pred. No. 8.9e-16;
 Matches 52; Conservative 40; Mismatches 73; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELLAEYQDLTTLTKQEIILAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60
 Db 1 MGTNTSSURPEVEEMQGTFTQKEIKLYKFKKLDKDGNGTISK-----DEFLM 52
 QY 61 LPEKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDGDD 120
 Db 53 IPELAVNLVLRVVISIPDEN-GDGSVNFKEFTAAALSVFNAQDKORKLEAFKVDIDGD 111
 QY 121 GTLNREXLSRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVIRS 178
 Db 112 GYISNGELFTVLKMMVG----NNLSDVQLQIQIVDKTILEADEDDGDKISFEFAKTL 165

RESULT 4
 US-08-328-322-17
 ; Sequence 17, Application US/08328322

Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match 21.3%; Score 203.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 1.8e-14;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRLSELAEYDYLFLTKQETLLAHRFCCELLPOQRVSESLRAQVPEQLTS 60
DB 1 MGAAPSKIVGLLED---INFODELERLKRKMKLDROSSGSIDKN-----EFMS 48
QY 61 LPELKANPFEICRYVSTSPAKDSLFEDFLDLVSFSDTAPDPIKSHVAFRIFFDD 120
DB 49 IPGVSSNPLAGRIWEVDADNSGD-VDFQFETIGLSIFSGSGKDEKLRFKITYDIDKD 107
QY 121 GTINREXLSLVNCLGEGEDTSLASSEMQLDNIIEESDIDRGTINLSEFOHVI 177
DB 108 GFISNELFLVKIMVG---SNLDEQLQOIVDRITVENDSDGDGRLSPEEFKNAI 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match 20.1%; Score 192.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 2.4e-13;
Matches 42; Conservative 40; Mismatches 59; Indels 13; Gaps 3;

QY 24 KOEILLARHRCCELLPOQRVSESLRAQVPEQLSLPELKANPFEICRYVSTSPAK 83
DB 3 RDEIERLKRKRFKMLDRDSSGSIDKN-----EFMSIPGVSSNPLAGRIWEVDADNSG 54
QY 84 DSLSEDFDLVSFSDTAPDPIKSHVAFRIFFDDGTINREXLSRVNCLTGEEDTR 143
DB 55 D-VDFQFETIGLSIFSGSGKDEKLRFKITYDIDKDFISNGELFLVKIMVG---SN 109
QY 144 LASEMQLDNIIEESDIDRGTINLSEFOHVI 177
DB 110 LDDEQLQOIVDRITVENDSDGDGRLSPEEFKNAI 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Nak, Uhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-720-625-4

Query Match 19.4%; Score 185.5; DB 4; Length 169;
Best Local Similarity 31.1%; Pred. No. 1.5e-12;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;
QY 56 EQILSLPELKPANPKERICRVFTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
DB 40 EEFMSLPQLQNPVLRVIDIFDTD-GNGEVDFKEFIEGVQSFSVKGKEQKLRFAPRIY 98
QY 116 DFDDGTLNREXLRLVNCGLTGEEDTRLSASEMKQLDNLILEESDIDRDTINLSEFQH 175
DB 99 DMDKDGYSINGELFQVLKMWG-----NNLKDQLQOIYDKTIINADKDGGRISFEFCA 154
QY 176 VI 177
DB 155 VV 156

RESULT 7
US-08-764-563-5
Sequence 5, Application US/08764563
Patent No. 6093565
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08764,563
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0178 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 461682
US-08-764-563-5

Query Match 19.4%; Score 185.5; DB 3; Length 170;

Best Local Similarity 31.1%; Pred. No. 1.5e-12;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;
QY 56 EQILSLPELKPANPKERICRVFTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
DB 41 EEFMSLPQLQNPVLRVIDIFDTD-GNGEVDFKEFIEGVQSFSVKGKEQKLRFAPRIY 99
QY 116 DFDDGTLNREXLRLVNCGLTGEEDTRLSASEMKQLDNLILEESDIDRDTINLSEFQH 175
DB 100 DMDKDGYSINGELFQVLKMWG-----NNLKDQLQOIYDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 8
US-08-655-352-8
Sequence 8, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequenin
DESCRIPTION: (Gen2:Drofreg) with homology to lily
DESCRIPTION: CCaMK
US-08-655-352-8

Query Match 18.3%; Score 175; DB 3; Length 186;
Best Local Similarity 25.4%; Pred. No. 2.4e-11;
Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 5;

QY 1 MGGSGSRLSKLLAEYQDLFTLTKOELLARHRECELLPOEQRVTSLSRAQVPEQILS 60
DB 1 MGKSSKLKODTIDRLTDTTFTTEKEIRQWHKGLKCPNGLLLEQGFQFIKYKQF-----55

QY 61 LPELANPKEKICRVSTSPAKDLSFEDFLDLSVFSDTATPDIKSHVAFRIFFDD 120
 Db 56 FPGDPSKFAVLVPRVDEN-NDGSIFFEFIRALSVTSKGL--DEKLOMARLYVDND 112
 QY 121 GTLNREXLSRLVNC-----TGEGETRLSASEMKOLINILEESIDIDGTINLSE 172
 Db 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PKRVKIDPDQMDKNHDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 9
 US-09-258-016-8
 ; Sequence 8, Application US/09258016
 ; Patent No. 6362395
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachettira W. Poovalah, Zhinua Liu,
 ; APPLICANT: Shameekumar Patil, Daisuke Takezawa
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
 ; ADDRESSEE: Whinston, LLP
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; STREET: Suite 1600
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/258, 016
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephens Jr., Donald L.
 ; REGISTRATION NUMBER: 34,022
 ; REFERENCE/DOCKET NUMBER: 4630-51994
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ. ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 186 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: Region of Drosophila frequenlin
 ; (gen2:Drofreq) with homology to 111y
 ; DESCRIPTION: CCAMK
 ; US-09-258-016-8

Query Match 18.3%; Score 175; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 2.4e-11;
 Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 5;

QY 1 MGGSGRLSKELAEYODLFTLKQETLLAHRFCCLPQEQRTVSSLRQVFFQILS 60
 Db 1 MGKSSKRLKQDTIDRLTDTYFTEKEIRQMHKGLKDCPNGLTDEGFIKYKF----- 55
 QY 61 LPELANPKEKICRVSTSPAKDLSFEDFLDLSVFSDTATPDIKSHVAFRIFFDD 120
 Db 56 FPGDPSKFAVLVPRVDEN-NDGSIFFEFIRALSVTSKGL--DEKLOMARLYVDND 112

QY 121 GTLNREXLSRLVNC-----TGEGETRLSASEMKOLINILEESIDIDGTINLSE 172
 Db 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PKRVKIDPDQMDKNHDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 10
 US-09-257-825B-8
 ; Sequence 8, Application US/09257825B
 ; Patent No. 6403352
 ; GENERAL INFORMATION:
 ; APPLICANT: Poovalah, Bachettira W.
 ; APPLICANT: Patil, Shameekumar
 ; APPLICANT: Takezawa, Daisuke
 ; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plant
 ; FILE REFERENCE: 4630-51993
 ; CURRENT APPLICATION NUMBER: US/09/257, 825B
 ; CURRENT FILING DATE: 1999-02-25
 ; PRIOR APPLICATION NUMBER: US 08/655,352
 ; PRIOR FILING DATE: 1996-05-23
 ; PRIOR APPLICATION NUMBER: US 60/014,743
 ; PRIOR FILING DATE: 1996-03-28
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 ; US-09-257-825B-8

Query Match 18.3%; Score 175; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 2.4e-11;
 Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 5;

QY 1 MGGSGRLSKELAEYODLFTLKQETLLAHRFCCLPQEQRTVSSLRQVFFQILS 60
 Db 1 MGKSSKRLKQDTIDRLTDTYFTEKEIRQMHKGLKDCPNGLTDEGFIKYKF----- 55
 QY 61 LPELANPKEKICRVSTSPAKDLSFEDFLDLSVFSDTATPDIKSHVAFRIFFDD 120
 Db 56 FPGDPSKFAVLVPRVDEN-NDGSIFFEFIRALSVTSKGL--DEKLOMARLYVDND 112
 QY 121 GTLNREXLSRLVNC-----TGEGETRLSASEMKOLINILEESIDIDGTINLSE 172
 Db 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PKRVKIDPDQMDKNHDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 11
 US-08-764-563-4
 ; Sequence 4, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; STATE: CA
 ; CITY: Palo Alto
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 109612
; US-08-764-563-4

Query Match      17.9%; Score 171.5; DB 3; Length 179;
Best Local Similarity 27.8%; Pred. No. 5.5e-11;
Matches 42; Conservative 30; Mismatches 66; Indels 13; Gaps 3;

QY 35 CELLPEQ-----RTVESLRQVPEQILSPKLNKPFKRICRVSTSPAKSL 86
Db 12 CNHDFEEIRRGKSRKLDLKSGLSIEEFMRPLQONPLVGRVIDFTD-GNGEV 70
QY 87 SPEDFDLLSVFSDATPIKSHYAFRIFDDGTLNREXLSRLVCLTGEGEDTRLSA 146
Db 71 DFHEFVGVTSQSVRGDEQKLRFAFRIVDMNDGFIENGELFQVLKMMVG----NNLKD 126
QY 147 SEMKQIDNILESDIDRGDTNLSEFQHV 177
Db 127 WOLQQLVDRKSLVLDKRGDGRISFEFSDV 157

RESULT 12
US-09-048-889-1
; Sequence 1, Application US/09048889
; Patent No. 6117989
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lal, Preeti
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,889
; FILING DATE: Herewith

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Certone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0493 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT09
; CLONE: 1846517
; US-09-048-889-1

Query Match      15.9%; Score 152.5; DB 3; Length 196;
Best Local Similarity 23.3%; Pred. No. 7.3e-09;
Matches 44; Conservative 39; Mismatches 73; Indels 33; Gaps 6;

QY 5 GSRLSKELLAEOYL----TFLTKQELLAHRRFCLELLPQEQRTVSSLRQVFFEQILS 60
Db 2 GSRTSHAAVDPDGSIRRETGFSQASLLRLHRRF-----RALDRNKKGYLSRMDLQ 53
QY 61 LPELKANFKERICRVSTSPAKSLSFDFDLDSVF-----SDPATPDIKS----- 108
Db 54 IGALAVNPLGDRIIIESFFPG-GSQRVDFPGFVRLAHFRPEDEDTQDPKKPEPLNSR 112
QY 109 ----HYAFRIFDDGTLNREXLSRLVCLTGEGEDTRLSASEMKQIDNILESDIDR 164
Db 113 RNKLHYAQLYLDDRGKISRHEMLQVLRMMVG-----VOVTEQLENIADRTVOEAD 168
QY 165 DGTINLSEF 173
Db 169 DGAVSFVEF 177

RESULT 13
US-08-655-352-3
; Sequence 3, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiyah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; CLASSIFICATION: 800

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural vistin-like protein
DESCRIPTION: (Gen2:Ratvnp3) with homology to 11ly
US-08-655-352-3

Query Match
Best Local Similarity 24.5%; Score 149; DB 3; Length 193;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELIAEYODLFTLKOEILAHRRFCCELLPOEORTVSSSLRAQVPEQILS 60
DB 1 MKONSKRLAPEVLQDLREHTEFTDHELOEWYKGFLLKDCPTGHLTVDE-----FKKIYA 53
QY 61 --LPELANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHAFRIEFD 118
DB 54 NEFPYGDSKFAEHVFRFTDIN-SDGTIDREFITLSTVS-RGKLEQKIKMAFSMYDLD 111
QY 119 DDCGLNREXLSRLVNCITGSGEDTRLASSEM-----QIDNLESDDIDROGTIN 169
DB 112 GNGYISSEMLEIVQAI-----YKMWSVMKMPEDESTPEKRTDKIFROMDINDOKLS 165
QY 170 LSEF-----QHVISRSPDFASSF 187
DB 166 LEEFIKGAKSDPSIVRLQCDPSSASQF 193

RESULT 14
US-09-258-016-3
Sequence 3, Application US/09258016
Patent No. 6362395
GENERAL INFORMATION:
APPLICANT: Bachettlira W. Poovaiyah, Zhinhua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kiarquist, Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S W Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.

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REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural vistin-like protein
DESCRIPTION: (Gen2:Ratvnp3) with homology to 11ly
US-09-258-016-3

Query Match
Best Local Similarity 24.5%; Score 149; DB 4; Length 193;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELIAEYODLFTLKOEILAHRRFCCELLPOEORTVSSSLRAQVPEQILS 60
DB 1 MKONSKRLAPEVLQDLREHTEFTDHELOEWYKGFLLKDCPTGHLTVDE-----FKKIYA 53
QY 61 --LPELANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHAFRIEFD 118
DB 54 NEFPYGDSKFAEHVFRFTDIN-SDGTIDREFITLSTVS-RGKLEQKIKMAFSMYDLD 111
QY 119 DDCGLNREXLSRLVNCITGSGEDTRLASSEM-----QIDNLESDDIDROGTIN 169
DB 112 GNGYISSEMLEIVQAI-----YKMWSVMKMPEDESTPEKRTDKIFROMDINDOKLS 165
QY 170 LSEF-----QHVISRSPDFASSF 187
DB 166 LEEFIKGAKSDPSIVRLQCDPSSASQF 193

RESULT 15
US-09-257-825B-3
Sequence 3, Application US/09257825B
Patent No. 6403352
GENERAL INFORMATION:
APPLICANT: Poovaiyah, Bachettlira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Daisuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plant
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR APPLICATION NUMBER: US 60/014,743
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
TYPE: PRT
LENGTH: 193
ORGANISM: Rat
US-09-257-825B-3

Query Match
Best Local Similarity 24.5%; Score 149; DB 4; Length 193;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

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DB 1 MKONSKRLAPEVLQDLREHTEFTDHELOEWYKGFLLKDCPTGHLTVDE-----FKKIYA 53
QY 61 --LPELANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHAFRIEFD 118
DB 54 NEFPYGDSKFAEHVFRFTDIN-SDGTIDREFITLSTVS-RGKLEQKIKMAFSMYDLD 111

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Fri Jan 17 13:03:50 2003

mutl127.rapb

mutation at p52127

Page 1

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:28 ; Search time 11 seconds
(without alignments) 345.163 Million cell updates/sec

Title: MUT127

Sequence: 1 MGSGSRLSKELLAERQDLT.....EFQHVISRPFDPASSFKIVL 191

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Gap 10.0, Gapext 0.5

Search: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	955	99.8	191	10	US-09-878-454A-2	Sequence 2, Appl1
2	943	98.5	191	12	US-10-109-885-2	Sequence 2, Appl1
3	338	35.3	187	10	US-09-802-116-2	Sequence 2, Appl1
4	183.5	19.2	170	12	US-10-109-885-3	Sequence 3, Appl1
5	176.5	18.4	195	10	US-09-999-602-3	Sequence 3, Appl1
6	171.5	17.9	195	10	US-09-999-602-4	Sequence 3, Appl1
7	140	14.6	220	10	US-09-350-874-26	Sequence 4, Appl1
8	135	14.1	216	10	US-09-350-874-6	Sequence 4, Appl1
9	135	14.1	220	10	US-09-350-874-4	Sequence 4, Appl1
10	135	14.1	227	10	US-09-350-874-8	Sequence 4, Appl1
11	135	14.1	227	10	US-09-350-874-10	Sequence 4, Appl1
12	135	14.1	245	10	US-09-350-874-4	Sequence 8, Appl1
13	135	14.1	252	10	US-09-350-874-20	Sequence 10, Appl1
14	135	14.1	270	9	US-09-350-874-14	Sequence 10, Appl1
15	134	14.0	216	9	US-09-965-528-15	Sequence 14, Appl1
16	134	14.0	216	10	US-09-350-874-2	Sequence 15, Appl1
17	133.5	13.9	216	10	US-09-999-602-1	Sequence 2, Appl1
18	132	13.8	270	10	US-09-350-874-18	Sequence 18, Appl1
19	130	13.6	225	10	US-09-350-874-30	Sequence 30, Appl1

20	130	13.6	252	10	US-09-350-874-22	Sequence 22, Appl1
21	130	13.6	252	10	US-09-350-874-28	Sequence 28, Appl1
22	130	13.6	252	10	US-09-350-874-42	Sequence 28, Appl1
23	130	13.6	257	10	US-09-350-874-16	Sequence 16, Appl1
24	120	12.5	229	10	US-09-350-874-70	Sequence 49, Appl1
25	120	12.5	233	10	US-09-350-874-49	Sequence 49, Appl1
26	120	12.5	250	10	US-09-350-874-72	Sequence 72, Appl1
27	110.5	11.5	172	12	US-10-109-885-4	Sequence 4, Appl1
28	110.5	11.5	1210	10	US-09-922-217-692	Sequence 692, App
29	110.5	11.5	1210	10	US-09-922-217-692	Sequence 692, App
30	110.5	11.5	1210	10	US-09-922-217-692	Sequence 692, App
31	110.5	11.5	1548	9	US-10-025-380-1095	Sequence 692, App
32	110.5	11.5	1548	10	US-09-922-217-1095	Sequence 692, App
33	109	11.4	256	10	US-09-350-874-32	Sequence 1095, Ap
34	108.5	11.3	142	10	US-09-910-071-4	Sequence 32, Appl1
35	108	11.3	642	9	US-09-554-000-6	Sequence 4, Appl1
36	108	11.3	656	9	US-09-554-000-8	Sequence 6, Appl1
37	107	11.2	203	10	US-09-350-874-12	Sequence 8, Appl1
38	107	11.2	642	9	US-09-554-000-2	Sequence 12, Appl1
39	107	11.2	652	9	US-09-554-000-4	Sequence 2, Appl1
40	106	11.1	256	10	US-09-350-874-36	Sequence 36, Appl1
41	105.5	11.0	201	10	US-09-925-297-714	Sequence 714, App
42	104.5	10.9	159	10	US-09-910-071-5	Sequence 5, Appl1
43	99.5	10.4	139	10	US-09-864-761-34808	Sequence 34808, A
44	93.5	9.8	171	9	US-09-981-353-161	Sequence 161, App
45	92.5	9.7	90	10	US-09-826-589-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Appl1 Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montefiore, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match	Score 955;	DB 10;	Length 191;
Best Local Similarity	99.58;	Pred. No. 1.6e-81;	
Matches 190;	Conservative 0;	Mismatches 1;	Indels 0;
Gaps 0;			
QY	1	MGSGSRLSKELLAERQDLTFTKQELLAHRRFCCLPEQRTVSSLRAPVFFQIIS	60
DB	1	MGSGSRLSKELLAERQDLTFTKQELLAHRRFCCLPEQRTVSSLRAPVFFQIIS	60
QY	61	LPFLKANPFRERICRVFSSPAKDSLSFEDFDLTVSFDTPAPDIKSHAFRPFDDDD	120
DB	61	LPFLKANPFRERICRVFSSPAKDSLSFEDFDLTVSFDTPAPDIKSHAFRPFDDDD	120
QY	121	GTINRDLRLVNCLEGEEDTFLSSEKQDLNLESDDIDRODTINLSEFOHYSRS	180
DB	121	GTINRDLRLVNCLEGEEDTFLSSEKQDLNLESDDIDRODTINLSEFOHYSRS	180
QY	181	PDFASSFKIVL 191	
DB	181	PDFASSFKIVL 191	
RESULT 2			

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US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match      98.5%; Score 943; DB 12; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.6e-88;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MGGSGSRLSKELLAAYQDITFTLTKQBILLAHRFCFELLPOEQRSVSSSLRAQVPEQILS 60

QY 61 LPELKPANPKERICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDFDD 120
    |||||
DB 61 LPELKPANPKERICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDFDD 120

QY 121 GTLNRELSRLVNCLTGEGEDTRLSASEMKQLIDNLEESDIDRGTINLSFQHVIRS 180
    |||||
DB 121 GTLNRELSRLVNCLTGEGEDTRLSASEMKQLIDNLEESDIDRGTINLSFQHVIRS 180

QY 181 PDFASSFKIVL 191
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DB 181 PDFASSFKIVL 191

RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020082406A1 Human Kinase Interacting Protein and Polynu
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match      35.3%; Score 338; DB 10; Length 187;
Best Local Similarity 39.9%; Pred. No. 4.5e-27;
Matches 77; Conservative 42; Mismatches 62; Indels 12; Gaps 5;

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QY 1 MGGSGSRLSKELLAAYQDITFTLTKQBILLAHRFCFELLPOEQRTVSSSLRAQVPE 56
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DB 1 MGNKQTVTHEQLEAYQDCTFTFRKIMRLFYRQDLAPQLVPLDYTTCPD---VKVPYE 57

QY 57 OILSLPELKANPKERICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIED 116
    |||||
DB 58 LIGSPELKANDPFRORIAQVFS-EDGDGHTMTLDNFMFVSEMAPRDLKAYYAFKIYD 116

QY 117 FDDGDTLNRELSRLVNCLTGEGEDTRLSASEMKQLIDNLEESDIDRGTINLSFQHV 176
    |||||
DB 117 FNNDDYICAWDLEQTQVTKLT-RGE---LSAEVSVLCVKVLDGADGHDGRLSLEDFOQM 172

QY 177 ISRSPDFPASSFKI 189
    |||||
DB 173 ILRAPDFLSTFHI 185

RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND M
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match      19.2%; Score 183.5; DB 12; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.7e-11;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPKERICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRI 115
    |||||
DB 41 EEFMSLPELQONPLVQVRVIDIFDID-GNGEVDFKEFTEGVSVKQDKQKLRFAFRY 99

QY 116 DFDDGDTLNRELSRLVNCLTGEGEDTRLSASEMKQLIDNLEESDIDRGTINLSFQHV 175
    |||||
DB 100 DMDKDGYSINGELFQVLRKMMVG----NNLKDTQLQOIVDKTIINADKDGGRISFEFCA 155

QY 176 VI 177
    ||
DB 156 VV 157

RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

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Query Match      14.6%; Score 140; DB 10; Length 220;
Best Local Similarity 23.4%; Pred. No. 6,2e-07;
Matches 43; Conservative 45; Mismatches 82; Indels 14; Gaps

QY      11 ELAAYDDLFLLKQOEILLARRFCELLPOEORTVESISRAQYFEOLIS--LPETKANP 68
Db      41 EGLFOLQEQRFKTRKEQLVYRGFKNECP-----SGIYNENEFQIISQFPGDST 93
QY      69 FKERICAVFSISPAKDSLEDFLDLLSVFSDFATPDIKSHIAFRIFDFDDGTINREXL 128
Db      94 YATLENAFADTN-HDGSVSEDEVAGLSVTL-NGTVDDRLNMAFNLYDNRKDCITKEEM 151
QY      129 SRLVNC---LTGEGEDRLFASEMKOILILEESIDIDRBDGTINLSEPHYISRPPDRA 185
Db      152 LDIMKSTYDMAGKTYTALNEAPRHEVENFFQKMDRNKDGVAVTLEEFLESCQKDNIMR 211
QY      186 SFKI 189
Db      212 SMOL 215

RESULT 8
US-09-350-874-6
; Sequence 6, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,217
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333

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; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-6

Query Match 14.1%; Score 135; DB 10; Length 216;
Best Local Similarity 25.6%; Pred. No. 1.9e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELAEYQDLTFLTKQELLAHRRFCCLPQEQRTVSSLRQAQVPEQLS--LPELKANP 68
DB 37 EGLEQLAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFKQIYAQFFPHGDAST 89
QY 69 FKERICRVSTSPAKDSLSFEDLDLLSVFSDTATPDIKSHYAFRIFDDEGTLNREXL 128
DB 90 YAHYLFNAFDITQT-GSVKFEDEVLTALSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEF 173
DB 148 MDIVKAIYDMGKYTPYVLKEDTPRQHVDFVFFQKMDKNKGIVTLDEF 195

RESULT 9
US-09-350-874-24
; Sequence 24, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenglian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-24

Query Match 14.1%; Score 135; DB 10; Length 220;
Best Local Similarity 22.8%; Pred. No. 2e-06;
Matches 42; Conservative 46; Mismatches 82; Indels 14; Gaps 5;

QY 11 ELAEYQDLTFLTKQELLAHRRFCCLPQEQRTVSSLRQAQVPEQLS--LPELKANP 68
DB 41 EGLEQLAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFKQIYAQFFPHGDAST 93
QY 69 FKERICRVSTSPAKDSLSFEDLDLLSVFSDTATPDIKSHYAFRIFDDEGTLNREXL 128
DB 94 YATFLFNAFDITN-HDGSVSEDEVLTALSILL-RGTVDRLNWFNLYDINKDGCITKEEM 151
QY 129 SRLVNC---LTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFQVIRSPDFAS 185
DB 152 LDINKSYDMGKYTPYALREAPREHVESFFQKMDKNKGIVTLDEFIESCKDENIMR 211
QY 186 SFKI 189
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-10

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Db 212 SMQL 215

RESULT 10
US-09-350-874-8
; Sequence 8, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenglian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-350-874-8

Query Match 14.1%; Score 135; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 2.1e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELAEYQDLTFLTKQELLAHRRFCCLPQEQRTVSSLRQAQVPEQLS--LPELKANP 68
DB 48 EGLEQLAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFKQIYAQFFPHGDAST 100
QY 69 FKERICRVSTSPAKDSLSFEDLDLLSVFSDTATPDIKSHYAFRIFDDEGTLNREXL 128
DB 101 YAHYLFNAFDITQT-GSVKFEDEVLTALSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM 158
QY 129 SRLVNC---LTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEF 173
DB 159 MDIVKAIYDMGKYTPYVLKEDTPRQHVDFVFFQKMDKNKGIVTLDEF 206

RESULT 11
US-09-350-874-10
; Sequence 10, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenglian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-10

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Db 144 YATFLNFAFTN-HDGSVSFEDFVAGLSVL-RGTVDRLNWFNLYDLNKGCIKEEM 201
QY 129 SRLVNC---LTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFAS 185
Db 202 LDIMKSIYDMGKTYTPALREAPREHVESFFQKMDRNKDGVTIEEFIESCKDENIMR 261
QY 186 SFKI 189
Db 262 SMQL 265

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RESULT 15

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US-09-965-528-15
; Sequence 15, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda M.
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 3216587CD1
US-09-965-528-15

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Query Match 14.0%; Score 134; DB 9; Length 216;
Best Local Similarity 25.6%; Pred. No. 2.4e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELLAEYQDLFLTKQEILLAHRRFCELLPOEQRTVESLRAQVPFEQILS--LPFLKANP 68
Db 37 EGLEOLEAQNTKRELQVLYRGFKNECP-----SGVYNEDTFKQIYAQFPFHGDAST 89
QY 69 FKERICRVFTSPAKDSLSFEDFLDLISVFSDFATPDPIKSHYAFRPFDDDDGTINREXL 128
Db 90 YAHYLFNFAFTTQT--GSVKFEDEFVLTSLILL-RGTVHEKLRWTFNLYINKDGYINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEF 173
Db 148 MDIVKATYDMGKTYTPVLKEDTPRQHVDFVFFQKMDRNKKGIVTLDEF 195

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Search completed: January 17, 2003, 12:44:48
Job time : 11 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003: Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 30 seconds
(without alignments)
1311.833 Million cell updates/sec

Title: MUT127
Sequence: 1 MGSGSRLSKELLAEYQDLT.....EFQHVISRSPDFASSPKIYL 191

Scoring table: BLOSUM62 ;
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriophage:*
- 17: sp-archae:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406	42.4	311	5	Q93640
2	362	37.8	185	11	Q9D9N5
3	339	35.4	187	4	Q96077
4	337.5	35.3	206	5	Q9W205
5	270	28.2	54	6	Q9GLJ2
6	224.5	22.5	180	5	Q9G833
7	199	20.8	175	5	Q9U0X7
8	187	19.5	175	10	Q9LS47
9	186	19.4	175	10	Q93VF2
10	181.5	19.0	169	5	Q9NEN1
11	180.5	18.9	244	5	Q20804
12	179.5	18.8	189	5	Q9VNF9
13	177.5	18.5	170	5	Q9NKM7
14	177.5	18.5	170	5	Q9SP81
15	176	18.4	200	5	Q8SRF8
16	174.5	18.2	115	11	Q99LQ9

17	173.5	18.1	187	5	Q9VWX8	Q9VWX8 drosophila
18	168.5	17.6	175	3	Q9HDE1	Q9HDE1 cryptococcus
19	168.5	17.6	177	3	Q9HDD3	Q9HDD3 cryptococcus
20	168	17.6	274	10	Q9AMW4	Q9AMW4 oryza sativ
21	167.5	17.5	195	5	Q23643	Q23643 caenorhabd1
22	167.5	17.5	213	5	Q16343	Q16343 caenorhabd1
23	167.5	17.5	213	10	Q9LMB8	Q9LMB8 caenorhabd1
24	167	17.5	170	4	Q8WYJ4	Q8WYJ4 homo sapien
25	167	17.5	173	4	Q96LZ3	Q96LZ3 homo sapien
26	167	17.5	190	5	Q9NAY9	Q9NAY9 naegleria f
27	162.5	17.0	161	10	Q9AY39	Q9AY39 oryza sativ
28	161.5	16.9	226	10	Q81446	Q81446 arabidopsis
29	156	16.3	190	3	Q96V50	Q96V50 arabidopsis
30	156	16.3	180	3	Q8TGC0	Q8TGC0 magnaporthe
31	151	15.8	166	5	Q9N2Y1	Q9N2Y1 magnaporthe
32	151	15.8	225	10	Q8W5C8	Q8W5C8 oryza sativ
33	149.5	15.6	226	10	Q81447	Q81447 arabidopsis
34	148.5	15.5	213	10	Q81445	Q81445 arabidopsis
35	148	15.5	246	10	Q82641	Q82641 arabidopsis
36	145	15.2	192	10	Q81328	Q81328 arabidopsis
37	145	15.2	222	10	Q81223	Q81223 arabidopsis
38	143	14.9	191	4	Q9DM19	Q9DM19 homo sapien
39	140	14.6	29	11	Q99JY5	Q99JY5 homo sapien
40	139.5	14.6	153	5	Q9U5J0	Q9U5J0 trichomonas
41	139.5	14.6	160	5	Q9U5I9	Q9U5I9 trichomonas
42	135	14.1	216	11	Q9UJ57	Q9UJ57 mus musculu
43	135	14.1	220	4	Q9N560	Q9N560 homo sapien
44	135	14.1	220	4	Q9HD11	Q9HD11 homo sapien
45	135	14.1	220	11	Q9JM60	Q9JM60 rattus norv

ALIGNMENTS

RESULT 1

Q93640 PRELIMINARY; PRT; 311 AA.

AC Q93640; 01-FEB-1997 (TREMREL. 02, Created)

DT 01-FEB-1997 (TREMREL. 02, Last sequence update)

DT 01-JUN-2002 (TREMREL. 21, Last annotation update)

DE F30A10.1 protein.

GN F30A10.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RA [1]

RA [1]

RA [1]

RA [1]

RA [1]

RA [1]

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RA [1]

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RA [1]

RA [1]

RA [1]

RA [1]

RA [1]

QY 1 MGSGSRLS-----KLLAEYQDLTFTTQELLAHRRCELLPOEQRVSS 48

DB 111 MGNASSLSLELNFSGVFTFQDLDEYDCFTFRKDIIRLYKRYVALNPKR---VPTN 167

Query Match 42.4%; Score 406; DB 5; Length 311;

Best Local Similarity 42.0%; Pred. No. 9.3e-29;

Matches 87; Conservative 41; Mismatches 53; Indels 26; Gaps 5;

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Db      68 DRICRVSHD---NVFSEFDVLGMASVFSGAQCPSLKIEYAFRIYDFNENGFTDEEDLEE 120
Qy     131 LVNLTGEGEDTRLASASE--MKQLIDNILEESDIDRDTGTINLSFEQHVIRSRSPDFASSFK 188
       :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db     125 IIVRLK-KSDD-ASDDLMDVHHVLESOLDNDMSLTSFSEFHMAKSPDFMNSFR 179
Qy     189 I 189
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Db     180 I 180

RESULT 3
Q96Q77 PRELIMINARY; PRT; 187 AA.
AC Q96Q77;
ID Q96Q77;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE KIP3.
GN KIP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayashi A., Okaze H., Kozuma S., Saito T.;
RT "KIP3.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EML; AB050868; BAB71789.1; -.
DR InterPro; IPRO02048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF-HAND; UNKNOWN.2.
DR PROSITE; PS00018; EF-HAND; UNKNOWN.2.
SQ SEQUENCE 187 AA; 21801 MW; FB3ZCCB46DF5ADCF CRC64;

Query Match          35.4%; Score 339; DB 4; Length 187;
Best Local Similarity 39.4%; Pred. No. 5.5e-23;
Matches 76; Conservative 42; Mismatches 63; Indels 12; Gaps

Qy     1 MGSGSRLSKELAEYQDLTFLLKQETLLAHRRFCLELPQ----EORTVESSLRQAQVPFE 56
       || :| | :| | ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db     1 MGNNQTVTHEQEAYODCFFTKRKETMRLFYIQDLAPQLVDLYTTCPD---VKVPYE 57
       ||| ||||| ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy     57 QILSLPELKNPKERICKRVSTSPAKDSLSFEDFLDLLSVFSDDTATPDIKSHYAIFRD 116
       ||| ||||| ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db     58 LIGSMPLKPNPQRQAQVS-EDGGHTLNFLDMFSYMSEMAPRDLKAYAKFIYD 116
       ||| ||||| ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy     117 FDDDGTLNRXLRLNCLTGEGEDTRLASAMKQIDMLESDIDRDTGTINLSFOHV 176
       :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db     117 FNNDYICAMDLEQTVTKLTRG-----LSAAEEVSLVCERKVLDEADGDHGRSLSEDFQNM 172
       :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy     177 ISRSPDFASSFKI 189
       | | | | | | | |
Db     173 ILRAPDFLSTFHI 185

RESULT 4
Q9W2Q5 PRELIMINARY; PRT; 206 AA.
AC Q9W2Q5;
ID Q9W2Q5;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE CG9236 protein.
GN CG9236.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phryganea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Cejnkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Mandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Abell J.F., Asprayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
RA Borokva D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Cantor A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., Moleod M.P., Moperson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puft V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson R., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissendach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan Q., Zhao Q., Zheng L.,
RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
EMBL: AE003452; AAF46635.1; -.
DR HSSP: Q99828; IDGV.
DR FLYbase: FBgn0034558; CG9236.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF000036; ehand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; EFh; 3.
DR PROSITE: PS00018; EF_HAND; 2.
KW Calcium-binding.
KW SEQUENCE 206 AA; 23591 MW; B3105F7F0F475A9 CRC64;

Query Match 35.3%; Score 337.5; DB 5; Length 206;
Best Local Similarity 43.8%; Pred. No. 8.6e-23;
Matches 77; Conservative 31; Mismatches 51; Indels 17; Gaps 5;

OY 17 QDILFLKQILLAHRRCELLQ---EQRTVESLSAQVPFEDILSLPELKAMPFERI 73
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
43 KDCFTFRKILVHKFKFRLRPDLVPRMTEGASVVKCECIEMPELR----- 94

OY 74 CRFVSTSPARDSLFEFDLLSVSDTATPDIKSHAFRIEDDDGTLNREXLSRLVN 133
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
95 -EAFSND-CGGNLSFEDFDLALSVFSQAPRDIVFAFKIYDPOGFIH---ADLMS 149

OY 134 CLTGEEDTFLSASEMKQILDNIIESDIDRDGTINLSEFOHVISRSPDASSFKI 189
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
150 CLTTMTKN-ELSPBEHQIADKVEADVDDGDKLSILEFEHVILRAPDFLSTHI 204

RESULT 5
O9GLJ2 PRELIMINARY; PRT; 54 AA.
AC O9GLJ2;
DT 01-MAR-2001 (Tremblrel. 16, Created)

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DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE DNA-pk interaction-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA Kexrood C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267715; AAC25931.1; -.
DR HSSP: Q99828; IDGV.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF000036; ehand; 1.
DR ProDom: PD000012; EF-hand; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1 54
FT NON_TER 1 54
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

Query Match 28.2%; Score 270; DB 6; Length 54;
Best Local Similarity 46.3%; Pred. No. 1.9e-17;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 102 ATPDKSHYAFRIEDDDGTLNREXLSRLVNCITGGEPTRLSASEMKQILDNI 155
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ATPDKSHYAFRIEDDDGTLNREXLSRLVNCITGGEPTRLSASEMKQILDNI 54

RESULT 6
O9GP83 PRELIMINARY; PRT; 180 AA.
ID O9GP83;
AC O9GP83;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Calcineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Alchem A.;
RC STRAIN-AX-2;
RL Thesis (2000), Department of Fachbereich Biologie,
RL Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RA Alchem A.;
RC STRAIN-AX-2;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ301668; CAC20026.2; -.
DR HSSP: P06705; LAUI.
DR InterPro: IPR002048; EF-hand.
DR ProDom: PD000012; RECOVERIN.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_3.
KW SEQUENCE 180 AA; 20739 MW; E2E947EBD280DOB6 CRC64;

Query Match 23.5%; Score 224.5; DB 5; Length 180;
Best Local Similarity 29.8%; Pred. No. 1.2e-12;
Matches 53; Conservative 43; Mismatches 67; Indels 15; Gaps 4;

OY 1 MGSGSRLSKELAEYDDLFITKQELLAHRRCELLQEQRTVESLSAQVPFEDILS 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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[illegible]

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RA C10i1 D Klinkert M.O.;
RA "Molecular cloning of Schistosoma mansoni calicleurin subunits and
RT immunolocalization to the excretory system.";
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL: AJ276885; CAB93677.1; -.
DR HSSP: P06705; 1TGO.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match 19.0%; Score 181.5; DB 5; Length 169;
Best Local Similarity 30.1%; Pred. No. 8,5e-09;
Matches 37; Conservative 31; Mismatches 50; Indels 5; Gaps 2

QY 56 EQILSLPELKPANPFERICRVEFTSPAKDSLSEDFDLILSVFSPTATPDIKSHVAFRIE 115
DB 40 KEFSLPELQNPVLAARVIEIPDTD-GNGEYDPKEKERNMSPGSAKGEAKLKFAFKIY 98
QY 116 PDDDDGTLRELKSLVNCVTGEGEDTRLSASEMKOLINIIIESDIDPDGNTINLSEFOH 175
DB 99 DMDKDGYSINQELFQVLKMWG-----NNLKPDQLOQIYDKTIMFPDKEDGRISFEFCE 154

QY 176 VLS 178
DB 155 VVS 157

RESULT 11
Q20804 PRELIMINARY; PRT; 244 AA.
AC Q20804;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAR-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE F55C10.1 protein.
GN F55C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z74036; CA98489.2; -.
DR HSSP: P06705; IAVI.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 244 AA; 27901 MW; 6899C858CB77D08B CRC64;

Query Match 18.9%; Score 180.5; DB 5; Length 244;
Best Local Similarity 27.8%; Pred. No. 1.7e-08;
Matches 50; Conservative 37; Mismatches 70; Indels 23; Gaps 6;

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[illegible]

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DB 2 GNENSLPMLCSNFD-----PDEIKRLGKRF-----RKLDLDSGSLSVDEEMTLP 47
OY 63 ELKANPFERICRVFSTSPAKDLSPEDELDLSVSDTATPDIKSHVAFRIFFDDOGT 122
DB 48 ELQONPLVQRYVIDFD-GNGEVPFKEITEGSVQSVKDKLSKIRFKIYDMKDKY 106
OY 123 LNREXLSRLVNCLTGEGEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVI 177
DB 107 ISNGELFOVLKMMVG-----NNLKDPLOLOIYKTIHADADGKISFEFCANV 157

RESULT 14
ID 095P81 PRELIMINARY: PRT: 170 AA.
AC 095P81;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcineurin B.
GN CNB.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHUKO X RYUHAJU, TISSUE=PIEROMONE GLAND;
RA Yoshiga T., Matsumoto S.;
RT "cDNA cloning of heterosubunits of calcineurin from pheromone gland of
  Bombyx mori."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF287251; AAK83039.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; EF-hand; 4.
DR ProDom: PD000012; EF-hand; 2.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
SO SEQUENCE 170 AA; 19357 MW; 5ECC15B820097130 CRC64;

Query Match 18.5%; Score 177.5; DB 5; Length 170;
Best Local Similarity 24.7%; Pred. No. 2e-08;
Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;

OY 3 GSGRLSKELAEYQDLFTKQELLHARRCELLPOQRVRESSLRQVFEQILSLP 62
DB 2 GNENSLPMLCSNFD-----ADEIRRLGKRF-----RKLDLDSGSLSVDEEMTLP 47
OY 63 ELKANPFERICRVFSTSPAKDLSPEDELDLSVSDTATPDIKSHVAFRIFFDDOGT 122
DB 48 ELQONPLVQRYVIDFD-ADNGEVPFKEITEGSVQSVKDKLSKIRFKIYDMKDKY 106
OY 123 LNREXLSRLVNCLTGEGEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVI 180
DB 107 ISNGELFOVLKMMVG-----NNLKDPLOLOIYKTIHADADGKISFEFCANV 160

RESULT 15
ID 08SRF8 PRELIMINARY: PRT: 200 AA.
AC 08SRF8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin beta subunit.
GN ECD08_0160.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryontidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barde V., Peyretallade E., Brothier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
  Encephalitozoon cuniculi."
RL Nature 414:450-453(2001).
DR EMBL: AL590448; CAD26322.1;
SO SEQUENCE 200 AA; 23929 MW; 3F0A4E2910E87701 CRC64;

Query Match 18.4%; Score 176; DB 5; Length 200;
Best Local Similarity 25.9%; Pred. No. 3.3e-08;
Matches 51; Conservative 40; Mismatches 80; Indels 26; Gaps 6;

OY 1 MGG-SGSRLSKELAEYQDLFTKQELLHARRCELLPOQRVRESSLRQVFEQIL 59
DB 1 MGSLSSTMLCEEIEELKMTTFVDEREIEHLTERF-QFLDRS-----RGILTYNEIN 52
OY 60 SLPKLANPFKRICRVFSTSPAKDLSPEDELDLSVSDTATPDIKSHVAFRIFFDD 119
DB 53 NIPFQSNPFSHLINKSIKMTDYKMTFPHLEFLGISEKNSKRNRIYLFDFDLNG 112
OY 120 DQTLNREXLSRLVNCLTGEGEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVI 179
DB 113 DRLCRNVLIRINKMK-----GQDGRVEAE-----NLNITYDEGGKGYLIDDFRYES 163
OY 180 SP-----DPASSF 188
DB 164 DPLIDKMTIDFSKMLK 180

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Search completed: January 17, 2003, 12:44:32
Job time : 32 secs


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; Sequence 2, Application US/09878454A
; GENERAL INFORMATION:
; APPLICANT: Monteiro, et al.
; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentlin
; FILE REFERENCE: 4115-161
; CURRENT APPLICATION NUMBER: US/09/878,454A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,939
; PRIOR FILING DATE: 2000-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-878-454A-2x
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DTRLSASEMKQIDNILESDIDRDGTINLSFQHVISRSPDFASSFKIVLI

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:19 ; Search time 36 seconds
(without alignments)
706.969 Million cell updates/sec

Title: US-09-878-454a-2x

Sequence: 1 MGSGSGRLSKELLAEYODLT.....EFQHVIRSPDFASFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875	96.8	191	AAW51215	Amino acid sequenc
2	869	96.1	191	AAW62287	Human protein phos
3	867	95.9	191	AAW64199	Human interferon r
4	328	36.3	172	AAU87324	Novel centril nerv
5	328	36.3	184	AAW43562	Human polypeptide
6	326	36.1	185	AAW4418	Amino acid sequenc
7	311	34.4	173	AAW56054	Human testicular a
8	311	34.4	173	AAU87612	Novel central nerv
9	311	34.4	173	AAW53662	Human reproductive
10	311	34.4	173	AAW43637	Human polypeptide

X at p5N5 116-128

11	311	34.4	173	22	AAU19952	Novel human calcin
12	309	34.2	187	22	AAE09736	Human kinase inter
13	297.5	32.9	206	22	ABW64325	Drosophila melanog
14	220	24.3	120	24	AAV11976	Human 5' EST seque
15	200.5	22.2	169	23	ABP41194	Human ovarian anti
16	164.5	18.2	175	20	AAU00881	Calcineurin regula
17	164	18.1	175	21	AAU21178	Zea mays protein f
18	164	18.1	210	21	AAU21177	Zea mays protein f
19	161	17.8	175	23	AAU51586	Arabidopsis thalia
20	161	17.8	175	23	ABW92357	Arabidopsis thalia
21	159	17.6	175	21	AAU07824	Human calcineurin
22	152	16.8	169	21	AAU51587	Herbicidally activ
23	150	16.6	169	21	AAU51587	Arabidopsis thalia
24	150	16.6	169	21	AAU51587	Arabidopsis thalia
25	146.5	16.2	170	19	AAW64200	Human calcineurin
26	146.5	16.2	170	21	AAU09978	Zea mays protein f
27	133.5	14.8	162	22	ABW55554	Human calcineurin
28	132.5	14.7	170	22	ABW60493	Drosophila melanog
29	130.5	14.4	226	21	AAU47032	Arabidopsis thalia
30	130	14.4	170	21	AAU09977	Human CBRI protel
31	130	14.4	170	22	AAU14411	Calcineurin B subu
32	130	14.4	173	22	AAW64410	Amino acid sequenc
33	130	14.4	187	22	AAU87337	Human testicular n
34	130	14.4	189	22	ABW5936	Human testicular n
35	130	14.4	189	22	AAU87615	Novel central nerv
36	130	14.4	189	22	AAU87615	Human reproductive
37	130	14.4	189	22	AAW43564	Human polypeptide
38	130	14.4	189	22	AAW43639	Human polypeptide
39	130	14.4	189	22	AAU19951	Novel human calcin
40	130	14.4	189	22	AAU19951	Human calcineurin
41	130	14.4	214	20	AAU31625	Human colon cancer
42	129.5	14.3	257	22	AAU51586	Arabidopsis thalia
43	127	14.0	226	21	AAU21763	Human ORFX ORF1575
44	126.5	14.0	201	21	AAU41811	Drosophila melanog
45	126.5	14.0	187	22	ABW61857	Drosophila melanog

ALIGNMENTS

RESULT 1	AAW51215	AAW51215 standard; Protein; 191 AA.
ID	AAW51215	
XX	AAW51215	
AC	AAW51215	
XX		
DT	21-AUG-1998	(first entry)
XX		
DE	Amino acid sequence of the calcium-integrin binding protein.	
XX		
KW	Human calcium-integrin binding protein; CIB; Integrin alpha IIB;	
KW	cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;	
KW	inhibition; blood coagulation; vascular disorder.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	116..128
FT		/note="EF-hand motif"
FT	Region	160..173
FT		/note="EF-hand motif"
XX		
PN	MO9814471-AL.	
XX		
PD	09-APR-1998.	
XX		
PF	24-SEP-1997;	97WO-US16828.
XX		
PR	02-OCT-1996;	96US-0720625.
XX		
PA	(UNIC-) UNIV NORTH CAROLINA.	
XX		
PI	Naik UP, Parise LV;	

XX WPI: 1998-240018/21.
 DR N-PSDB; AA07211.
 XX
 PT New isolated calcium-integrin binding protein - is expressed in
 PT platelets and activates the fibrinogen receptor, used to develop
 PT products for treating e.g. vascular disorders
 XX
 PS Claim 1; Page 30; 44pp; English.
 XX
 CC This is the amino acid sequence of the human calcium-integrin binding
 CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
 CC domain. The CIB protein is expressed in platelets and interacts with
 CC the alpha IIB subunit of integrin alpha IIB-beta 3, to activate the
 CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
 CC activation of the fibrinogen receptor where it is desired to reduce
 CC blood coagulation for therapeutic, diagnostic or pharmaceutical
 CC reasons. The products can be used for treating vascular disorders,
 CC and for isolating or purifying integrins or fibrinogen. They can also
 CC be used for detection and diagnosis.
 XX
 SQ Sequence 191 AA;
 Query Match 96.8%; Score 875; DB 19; Length 191;
 Best Local Similarity 92.7%; Pred. No. 2.2e-98;
 Matches 177; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MGGSGRLSKELLAQYQDLTFTKQELLAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
 DB 1 MGGSGRLSKELLAQYQDLTFTKQELLAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
 QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVLCNLTGEGEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISRS 180
 DB 121 GTLNREDLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 2
 AAW62287
 ID AAW62287 standard; Protein; 191 AA.
 XX
 AC AAW62287;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Human protein phosphatase regulatory subunit.
 XX
 KW Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
 KW immunosuppression; neurodegeneration; inflammation; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 44
 FT /label- unknown
 FT /note- "encoded by ASG"
 FT Misc-difference 45
 FT /label- unknown
 FT /note- "encoded by TGN"
 XX
 PN W09826056-A1.
 XX
 PD 18-JUN-1998.
 XX
 PF 25-NOV-1997; 97WO-US21603.
 XX

PR 12-DEC-1996; 96US-0764563.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Goll SK, Hillman JL;
 XX
 DR WPI: 1998-348518/30.
 DR N-PSDB; V398009.
 XX
 PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
 PT prevention and treatment of immuno-suppression, neuro-degeneration,
 PT inflammation and cancer
 XX
 PS Claim 1; Fig 1; 65pp; English.
 XX
 CC The present sequence is a pure human protein phosphatase regulatory
 CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
 CC HCNB, are used to produce recombinant HCNB which is used to treat or
 CC prevent immunosuppression or neurological diseases (especially parasitic,
 CC bacterial or viral infections, including AIDS; the effects of radio- or
 CC chemo-therapy and Alzheimer's disease). Antagonists which bind
 CC specifically to HCNB and modulate its activity are used to treat
 CC inflammation, cancer, or immunological disorders and allograft rejection
 CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
 CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
 CC arthritis). Complements of the DNA encoding HCNB are useful as probes
 CC and primers for detecting the DNA encoding HCNB by hybridisation or
 CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
 CC particularly for diagnosis of the specified disorders, including early
 CC diagnosis of cancers. The probes can also be used to map the
 CC corresponding genomic sequence, while Ab are also useful in drug
 CC screening and for purifying native HCNB. Therapeutic agents are
 CC administered orally, intravenously, intramuscularly, topically or
 CC rectally, normally at 0.1-105 mu g.
 XX
 SQ Sequence 191 AA;
 Query Match 96.1%; Score 869; DB 19; Length 191;
 Best Local Similarity 92.1%; Pred. No. 1.2e-97;
 Matches 176; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MGGSGRLSKELLAQYQDLTFTKQELLAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
 DB 1 MGGSGRLSKELLAQYQDLTFTKQELLAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
 QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVLCNLTGEGEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISRS 180
 DB 121 GTLNREDLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRGTINLSFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 3
 AAW64199
 ID AAW64199 standard; Protein; 191 AA.
 XX
 AC AAW64199;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Human interferon receptor 1 binding protein IR1B1.
 XX
 KW Interferon receptor 1 binding protein; IR1B1; human; tumour;
 KW cancer; gene therapy; tissue graft; graft survival.
 XX
 OS Homo sapiens.
 XX

PN W09831796-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 15-JAN-1998; 98MO-US00671.
 XX
 PR 15-JAN-1997; 97US-0035636.
 XX
 PA (MCIN/) MCINNIS P A.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Abramovitch C, Chebath JE, Revel M;
 DR WPI: 1998-414096/35.
 DR N-PSDB: AAV44272.
 XX
 PT New isolated interferon receptor binding proteins - used to develop
 PT products for modulating sensitivity to interferon, e.g. in the
 PT treatment of tumours or for prolonging graft survival
 XX
 PS Claim 1, Page 34; 64pp: English.
 XX
 CC This is a novel human protein, designated interferon receptor
 CC binding protein 1 (IRB1), which interacts with the intracytoplasmic
 CC (IC) domain of the IFNAR1 chain of the interferon type 1 (IFN-alpha,
 CC beta or omega) receptor. IRB1 is a new member of the calcineurin
 CC and calcitracin family of calcium-regulated proteins (see also
 CC AAM64200). It is induced very rapidly and transiently following IFN
 CC treatment of human cells. It was identified in a two-hybrid
 CC screening for proteins interacting with the IFNAR1-IC domain;
 CC another protein, IRB4 (see AAV44272) encoding IRB1, host cells and expression
 CC CDNA clone (see AAV44272) encoding IRB1, host cells and expression
 CC vectors are claimed. DNA encoding IRB1 and IRB4 can be used in
 CC result in a decrease in malignant cell growth and an enhanced
 CC response to exogenous IFN therapy. Antisense IRB1 or IRB4
 CC nucleic acids can be used for prolonging tissue or organ graft
 CC survival in patients as the rejection of these grafts in the host
 CC is mediated by the histocompatibility antigens (MHC class I) whose
 CC synthesis depends on the IFN stimulus. The products can also be
 CC used in detection and diagnosis.
 XX
 XX Sequence 191 AA;
 SQ
 Query Match 95.9%; Score 867; DB 19; Length 191;
 Best Local Similarity 92.1%; Pred. No. 2,1e-97;
 Matches 176; Conservative 1; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELAEYQDITFLTKQETILAHRRFCLELPOEORTVSSLRQVPEQIIS 60
 DB 1 MGSSGRLSKELAEYQDITFLTKQETILAHRRFCLELPOEORTVSSLRQVPEQIIS 60
 QY 61 LPELKNPKEKICRVFTSPAKDSLSEFDLILSVFSDTAPPDIKSHAFRIFXXXX 120
 DB 61 LPELKNPKEKICRVFTSPAKDSLSEFDLILSVFSDTAPPDIKSHAFRIFPPDD 120
 QY 121 XXXXXXXXRLVNCILGREGEDRLSASEMKQLINDLIESDIDROGTINLSEFOHVIS 180
 DB 121 GLINEDLSRLVNCILGREGEDRLSASEMKQLIDYILLESIDIDROGTINLSEFOHVIS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 4
 AA087324
 ID AA087324 standard; Protein; 172 AA.
 XX
 AC AA087324;
 XX
 DT 05-JUN-2002 (first entry)
 XX

DE Novel central nervous system protein #234.
 XX
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 OS
 XX Homo sapiens.
 XX
 FN W0200155318-A2.
 PN
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01332.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214686.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0228927.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 240.
DE
XX
KW Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; anticancer; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-0501309.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234999.
PR 26-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250300.
PR 01-DEC-2000; 2000US-0250301.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-488781/53.
XX N-PSDB; AAI63868.
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. The
XX genes were isolated from a range of human tissues disclosed in the
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
XX urogenital; (b) immune disorders e.g. Addison's disease, allergies,
XX autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 184 AA;
Query Match 36.3%; Score 328; DB 22; Length 184;
Best Local Similarity 40.7%; Pred. NO. 1.4e-31;
Matches 72; Conservative 31; Mismatches 64; Indels 10; Gaps 3;
QY 13 LAEYQDLTFTKQETLLAHRRCFCELLPQORTVESLRAQVPFEQILSLPELKANPFKE 72
DB 13 LEEYQALFTLRNEILCHIDFTLKLCPGKYKKEATL----TMDQVSSLPALRVNPFDR 68
QY 73 ICRVFTSPAKDSLSFEDFLDLVSVFSDTATPDIKSHYAFRIEFXXXXXXXSLRV 132
DB 69 ICRVFS---HKGMSFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 125
QY 133 NCLTGEEDTRLGASEMKQLIDNILESDIDRGTINLSEFQHVIRSPDFASSFKI 189
DB 126 LRLNLSDD---MSEDLMLDNLNHLVSEDLNDNMLSFSEFHAMAKSPDFMNSFRI 179
RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX AAB64418;
XX 22-MAR-2001 (first entry)
XX Amino acid sequence of human intracellular signalling molecule INTRA50.
XX Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
XX mental disorder; schizophrenia; anxiety.
OS Homo sapiens.
XX WO2000077040-A2.
XX 21-DEC-2000.
XX 16-JUN-2000; 2000WO-US16636.
XX 16-JUN-1999; 99US-0139566.
XX 17-AUG-1999; 99US-0149640.
XX 09-NOV-1999; 99US-0164417.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
XX WPI; 2001-025334/03.
XX N-PSDB; AAF32887.
XX New human intracellular signalling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX Claim 5; Page 158-159; 192pp; English.
XX Sequences AAF32638 - AAF32689 represent cDNA encoding human
XX intracellular signalling molecules INTRA1 - INTRA52, represented in
XX AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
XX of the invention exhibit immunosuppressive; cytostatic; neuroprotective;
XX nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
XX neuroleptic; antiarteriosclerotic; antifungal; antiviral; antiparasitic;
XX antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
XX agonists and antagonists are useful for the treatment of a condition
XX associated with decreased or increased expression of functional INTRA.
XX Disorders associated with abnormal INTRA expression or activity include
XX cell proliferative disorders e.g. arteriosclerosis and cancers;
XX autoimmune or inflammatory disorders e.g. Addison's disease and acquired
XX immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
XX protozoal and helminthic infections; gastrointestinal disorders e.g.
XX dysphagia and irritable bowel syndrome; neurological disorders e.g.
XX epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
XX disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
XX disorder. Antibodies immuno specific for the INTRA proteins may also be
XX useful in the diagnosis of the above disorders.
XX Sequence 185 AA;
Query Match 36.1%; Score 326; DB 22; Length 185;
Best Local Similarity 40.8%; Pred. NO. 2.4e-31;
Matches 73; Conservative 30; Mismatches 66; Indels 10; Gaps 3;
QY 11 ELAEYQDLTFTKQETLLAHRRCFCELLPQORTVESLRAQVPFEQILSLPELKANPFK 70
DB 12 EDLEEYQALFTLRNEILCHIDFTLKLCPGKYKKEATL----TMDQVSSLPALRVNPF 67
QY 71 ERICRVFTSPAKDSLSFEDFLDLVSVFSDTATPDIKSHYAFRIEFXXXXXXXSLRV 130
DB 68 DRICRVFS---HKGMSFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRI 124
QY 131 LVNCLTGEEDTRLGASEMKQLIDNILESDIDRGTINLSEFQHVIRSPDFASSFKI 189
DB 125 IILRLNLSDD---MSEDLMLDNLNHLVSEDLNDNMLSFSEFHAMAKSPDFMNSFRI 180
RESULT 7

AB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01329.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225219.
PR 14-AUG-2000; 2000US-0225214.
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 PR 08-DEC-2000; 2000US-0251869.
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 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483232/52.
 DR
 XX Nucleic acids encoding 973 human testicular antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating testicular cancer -
 XX
 XX Claim 11; SEQ ID NO 1438; 766pp; English.
 XX
 CC The present invention provides the protein and coding sequences of 973
 CC human testicular antigens, and fragments of their genomic sequences. The
 CC sequences can be used in the treatment of cardiovascular, urinary system,
 CC reproductive system, immune, respiratory, neurological and
 CC gastrointestinal disorders, infections, and particularly cancer,
 CC especially testicular cancers. The present sequence is a protein of the
 CC invention.
 XX
 XX Sequence 173 AA;
 SQ
 Query Match 34.4%; Score 311; DB 22; Length 173;
 Best Local Similarity 39.4%; Pred. No. 1.5e-29;
 Matches 69; Conservative 30; Mismatches 56; Indels 10; Gaps 3;
 Oy 13 LAEYQDLFLKQETLLAHRPCFELLPOEQTVESSLRQVFFQILSLPELKANPKFR 72
 Db 1 LEEYQALFLRNEITLCHDTFLKCPGKYKATL----TMDQVSSLPALRVNPFDR 56
 Oy 73 ICRVSTSPAKDSLFEDLLSVFSDTATPDIKSHVAFRIEXXXXXXXXSRLV 132
 Db 57 ICRVFS---HGKMSFEDVLGMSVFSQACPSLKIEFAFRIYDFNENGFDIEDLQRII 113
 Oy 133 NCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRPDFASSF 187
 Db 114 LRLNSDD---MSEDLMLDNLHVLXSDDLNDNMLSFSEFEHMAKSPDFMTFF 165
 RESULT 8
 AAU87612
 ID AAU87612 standard; Protein; 173 AA.
 XX
 AC AAU87612;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Novel central nervous system protein #522.
 XX
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX
 OS Homo sapiens.

XX
 PN WO200155318-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01332.
 XX
 PR 31-JAN-2000; 2000US-0179055.
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 PR 24-FEB-2000; 2000US-0184664.
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 PR 14-JUL-2000; 2000US-0218290.
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 PR 26-JUL-2000; 2000US-0220964.
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 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
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 PR 23-AUG-2000; 2000US-0227009.
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 PR 14-SEP-2000; 2000US-0232397.
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 PR 14-SEP-2000; 2000US-0233063.
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 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.

PI	Rosen CA; Barash SC; Ruben SM;
DR	WPI; 2001-581633/65.
XX	N-PSSB; ABRK3942.
PT	New isolated nucleic acid encoding a protein for diagnosing,
PS	preventing, treating or ameliorating medical conditions and used as
XX	food additives or preservatives -
XX	Claim 9; SEQ ID No 1130; 837pp; English.
CC	The invention describes an isolated nucleic acid molecule (I) encoding a
CC	novel central nervous system protein. (I) and polypeptides (II) encoded
CC	by (I), are used to treat a medical conditions and in diagnosis of a
CC	pathological condition. Disorders which are diagnosed or treated include
CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC	amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC	e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC	e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC	adenocarcinomas and irritable bowel syndrome, reproductive system
CC	disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC	and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC	leukaemia, disorders involving neovascularisation e.g. malignancies,
CC	respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC	acute kidney failure and blood related disorders e.g. myocardial
CC	infection. The polypeptides can also be used to aid wound healing and
CC	epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC	maintain organs before transplantation, for supporting cell culture of
CC	primary tissues, to regenerate tissues and in chemotaxis. The
CC	polypeptides can also be used as a food additive or preservative to
CC	increase or decrease storage capabilities, fat content, lipid, protein,
Query Match	34.4%; Score 311; DB 22; Length 173;
Best Local Similarity	39.4%; Pred. No. 1.5e-29;
Matches	69; Conservative 30; Mismatches 66; Indels 10; Gaps 3
QY	13 LAEYDUTRLTGOEILAHRRFCCELLPOQRVSSLRAQVPFEQILTSLPELKANPFKER 72
DB	1 LREYQALFELTNELLICIDDTFLKLCPPGKKYKEATL---TWDDQVSLPALRVNPFRR 56
QY	73 ICRVSTSPARKSLSPEDLDLTVSPSDPATPDIKSHVAFRIFFXXXXXXXSRLY 132
DB	57 ICRVTS---HKMFSEEDVLGMAYVFSEQACPSLKTETVFRIRYDFENEGFIDEDLQRTI 113
QY	133 NCLVGEDETRLSASEMKQLINDINEESIDDGTINTISEFOHVIYSRSPDEASSF 187
DB	114 LRLNSDD---MSEDLLMDLTNHVLSXSDLDNDNMISFEEFHAAKSSPDMFTPF 165
RESULT 9	
AAM95362	
ID	AAM95362 standard; Protein: 173 AA.
AC	AAM95362;
XX	
DT	21-NOV-2001 (first entry)
XX	
DE	Human reproductive system related antigen SEQ ID NO: 4020.
KW	Human; reproductive system related antigen; reproductive system disorder;
RV	cancer; gene therapy.
XX	
OS	Homo sapiens.
PX	
XX	WO200155320-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01339.

PR 31-JAN-2000; 2000US-0179065.
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 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX
 PI WPI; 2001-465570/50.
 XX N-PSDB; AAL01332.
 DR Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PT

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PR	08-NOV-2000	2000US-0246477
PR	08-NOV-2000	2000US-0246478


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PR 01-SEP-2000; 2000US-0229345.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 08-NOV-2000; 2000US-0246475.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249264.
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PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0256719.
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(PHMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM.
WPI: 2001-465568/50.
N-PSDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is
used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID No 149; 542pp; English.

The present invention relates to the isolation of novel human
calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
sequences encoding for these proteins. The sequences of the invention
are useful in the diagnosis, prevention and/or prognosis of diseases
associated with aberrant calcium flux. Such disorders include
neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
immune dysfunction (e.g. severe combined immunodeficiency, SCID),
digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
disease (e.g. cancer), blood infectious diseases (e.g. haemophilia), and/or
infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
novel calcium-binding proteins are also useful as screening tools to
identify antagonists and/or agonists that may enhance or inhibit
activities mediated by calcium-binding proteins. The polynucleotides of
the invention are also useful in gene therapy. AAU19892-AAU19969
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 173 AA;
Query Match 34.4%; Score 311; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 1,5e-29;
Matches 69; Conservative 30; Mismatches 66; Indels 10; Gaps 3;

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QY 13 LAEQDQLTFLTKOEILLAHRRFCELLPQRTVSSSLRAQVPEEQILSLPELKANPFKER 72
 DB 1 LEYQALTLTRNEILLIHTKLCPPGKYKEATL---TMDQVSSLPALRVNPFDR 56
 QY 73 ICRVFTSPAKDSLSPEDFLDLSVFSOTATPDIKSHYAFRIFFXXXXXXXXXXSRIV 132
 DB 57 ICRVFS---HKGMSFEDVLGNASVSEQACSLKIEAFRIYDNENGFIDEEDLQRI 113
 QY 133 NCLTGGEGTRLSASEMKOLINDILESDIDRGNTINSEFOHVSRSPPDFASSF 187
 DB 114 LRLANSDD---MSEDLMLDLTNHVLXSOLDNDNMLSFSEFEHAKSPDFWTFP 165

RESULT 12
 AAE09736
 ID AAE09736 standard; Protein; 187 AA.
 AC AAE09736;
 DT 29-NOV-2001 (first entry)
 DE Human kinase interacting protein.
 XX Human; kinase interacting protein; novel human protein; NHP;
 KW gene therapy; drug screening; mental disorder; biological disorder;
 KW medical disease; nootropic.
 XX Homo sapiens.
 OS WO200166760-A2.
 PN 13-SEP-2001.
 PD 08-MAR-2001; 2001WO-US07499.
 PF 08-MAR-2000; 2000US-0187719.
 PR (LEXI-) LEXICON GENETICS INC.
 PA Mathur B, Turner CA;
 PI WPI; 2001-557870/62.
 DR N-PSDB; RAD16796.
 XX Novel polynucleotides encoding human kinase interacting protein useful
 PT for drug screening, diagnosis and in gene therapy of biological
 PT disorders
 PS Claim 2; Page 31-32; 32pp; English.
 XX The present amino acid sequence is a novel human protein (NHP),
 CC human kinase interacting protein. NHP oligonucleotides are useful
 CC as hybridisation probes for screening libraries and assessing gene
 CC expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene are used to design primers for
 CC use in amplification assays to detect mutations within the exons,
 CC splice sites, introns that can be used in diagnostics and
 CC pharmacogenomics. NHP nucleotide sequences are useful for drug
 CC screening and nucleotide construct encoding NHP products are
 CC useful in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo.
 CC The encoded NHP polypeptides are useful for generating antibodies,
 CC as reagents in diagnostic assays, for identifying other cellular
 CC gene products related to NHP and as reagents in assays for screening
 CC for compounds that are useful in the treatment of mental, biological
 CC or medical disorders and diseases.
 XX Sequence 187 AA;

Query Match 34.2%; Score 309; DB 22; Length 187;
 Best Local Similarity 37.8%; Pred. No. 2.9e-29;
 Matches 73; Conservative 39; Mismatches 69; Indels 12; Gaps 5;

QY 1 MGGSGRLSKELLABYQDQLTFLTKOEILLAHRRFCELLPQ---EORTVSSSLRAQVPE 56
 DB 1 MGNKQVTFHEQLEAYQDCTFTTRKEIMRLFYRYQDLAQQLVPLDVTTCPD---VKVPYE 57
 QY 57 QILSLPELKANPFKERICRIVFSTSPAKDSLSPEDFLDLSVFSOTATPDIKSHYAFRI 116
 DB 58 LIGSMPELKDNPFRIQAQVFS-EDGDGHMTLDNFDLDFSVMSMAPRDLKAYYAEKIYD 116
 QY 117 XXXXXXXXXXSRIVNCLTGGEGTRLSASEMKOLINDILESDIDRGNTINSEFOHV 176
 DB 117 FNNDYICAWDLEQVTKLT-RGE---LSAEEVSIVCKEVLDEADGDHGRUSLEDFQNM 172
 QY 177 ISRSPDFASSEKI 189
 DB 173 ILRAPDFELSTFHI 185

RESULT 13
 ABB64325
 ID ABB64325 standard; Protein; 206 AA.
 AC ABB64325;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 19767.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL08428.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions
 PS Disclosure; SEQ ID NO 19767; 2lpp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA
 CC sequences (ABLO1840-ABLI6175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 206 AA;

Query Match 32.9%; Score 297.5; DB 22; Length 206;
 Best Local Similarity 40.9%; Pred. No. 8.5e-28;
 Matches 72; Conservative 30; Mismatches 57; Indels 17; Gaps 5;

QY 17 QDLTFLTKOEILLAHRRFCELLPQ---EORTVSSSLRAQVPEEQILSLPELKANPFKERI 73


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Db      43 KCCTFTTRKEILRVHKKREFELRPDLVPRMTEGQASVAVPCPCIEKMPELR----- 94
OY      74 CRVFSTPAKDSLFEDFDLISVSDTTPDIKSHYARIRKXXXXXXXSRLYN 133
Db      95 -EARSRD-GQGULSFEDFLDALSVSEQAPRDIKVFYARKI---DFDODGFIQHADLMS 149
OY      134 CLTGEDTRLSASEMKOLIDNILESDIDRDGTINLSFQVHYSRSPDFASSFKI 189
Db      150 CLTWTXN-ELSPEDHQIADKVIIEADVDGDKSLIEFEHVILRAPFLSTFRI 204

RESULT 14
AAV11976
ID      AAV11976 standard; Protein: 120 AA.
AC      AAV11976;
XX
XX      18-JUN-1999 (first entry)
XX
DE      Human 5' EST secreted protein SEQ ID NO: 576.
XX
KW      Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW      forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW      upstream regulatory sequence; cytokine activity; cell proliferation;
KW      differentiation; haematopoiesis regulation; tissue growth regulation;
KW      reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW      thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS      Homo sapiens.
XX
PN      WO9906550-A2.
XX
PD      11-FEB-1999.
XX
PE      31-JUL-1998; 98WO-IB01232.
XX
PR      01-AUG-1997; 97US-0905144.
XX
PA      (GEST ) GENSET.
XX
PI      Ducleert A, Dumas M,Ine Edwards J, Lacroix B;
XX      WPI; 1999-153780/13.
XX      N-PSDB; AAX40698.
XX
PT      New isolated prostate-derived nucleic acids - used to develop
PT      products which may have cytokine, immune regulatory, haematopoiesis
PT      regulating, anti-inflammatory or tumour inhibition activity
XX
PS      Claim 34; Page 664; 675pp; English.
XX
CC      AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC      human secreted proteins expressed in prostate, and encode the proteins
CC      given in AAV11716 to AAV11993 respectively. The proteins given represent
CC      the signal peptide and an N-terminal fragment of a secreted protein. The
CC      nucleic acid sequences can be used for producing secreted human gene
CC      products. They can also be used to develop products for diagnosis and
CC      therapy. The proteins obtained may have cytokine activity, cell
CC      proliferation and differentiation activity, haematopoiesis regulating
CC      activity, tissue growth regulating activity, reproductive hormone
CC      regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC      thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC      activity, tumour inhibition activity or other activities. The products
CC      can be used in forensic, gene therapy and chromosome mapping procedures.
CC      The sequences can also be used for obtaining corresponding promoter
CC      sequences. The nucleic acids encoding the signal peptides can be used for
CC      directing extracellular secretion of a polypeptide or the insertion of a
CC      polypeptide into a membrane, or importing a polypeptide into a cell.
XX
XX      Sequence 120 AA;
XX
Query Match      24.3%; Score 220; DB 20; Length 120.

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Best Local Similarity 66.2%; Pred. No. 1,2e-18;
Matches 45; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
OY      1 MCGSGSRLSKELLAEYQDITFLTKOELLAHRRFPELLPOEORTVSSIRAGVPEQILS 60
Db      1 MCGSGSRLSKELLAEYQDITFLTKOELLAHRRFPELLPOEORXXSRHGHCHCPSSRFA 60
OY      61 LEPIKAMP 68
Db      61 FOSSRPTP 68

RESULT 15
ABP41194
ID      ABP41194 standard; Protein: 169 AA.
AC      ABP41194;
XX
XX      23-AUG-2002 (first entry)
XX
DE      Human ovarian antigen HTLN94, SEQ ID NO:2326.
XX
KW      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW      ovarian cancer; breast cancer; reproductive system disorder;
KW      infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW      PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW      inflammatory condition; immune disorder; blood disorder;
KW      cardiovascular disorder; respiratory disorder; neurological disorder;
KW      gastrointestinal disorder; urinary system disorder; drug screening;
KW      gene therapy; chromosome mapping; forensic analysis;
KW      antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW      antiinflammatory; gynaecological; reproductive.
XX
OS      Homo sapiens.
XX
PN      WO200200677-A1.
XX
PD      03-JAN-2002.
XX
PE      07-JUN-2001; 2001WO-US18569.
XX
PR      07-JUN-2000; 2000US-209467P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Birse CE, Rosen CA;
XX
PT      WPI; 2002-147878/19.
PT      N-PSDB; ABQ54271.
XX
CC      Isolated nucleic acid molecules encoding novel ovarian polypeptides,
CC      useful in the prevention, treatment and diagnosis of cancer (e.g.
CC      neurological diseases -
CC      Claim 11; SEQ ID NO 2326; 2922pp; English.
XX
CC      The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC      ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC      encompasses polypeptides 90% identical and polynucleotides 95% identical
CC      to the sequences of the invention. The invention additionally relates to
CC      recombinant vectors and host cells comprising human ovarian antigen
CC      polynucleotides, antibodies against human ovarian antigens, and the use
CC      of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC      treating, prognosing or preventing various ovary and/or breast-related
CC      disorders. Such conditions include ovarian cancer and breast cancer, and
CC      metastatic tumours of ovarian or breast origin, reproductive system
CC      disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC      polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC      disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC      shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC      vaginitis), immune disorders (e.g., congenital and acquired
CC      immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

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Job time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:44:54 (Search time 14 Seconds)

(without alignments)
401.413 Million cell updates/sec

Title: US-09-878-454a-2x

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	869	96.1	191	3	US-08-764-563-1
3	176.5	19.5	177	3	US-08-764-563-3
4	164.5	18.2	174	1	US-08-328-322-17
5	153.5	17.0	157	1	US-08-328-322-15
6	146.5	16.2	169	4	US-08-720-625-4
7	146.5	16.2	170	3	US-08-764-563-5
8	130.5	14.4	176	3	US-08-655-352-8
9	126	13.9	186	4	US-09-258-016-8
10	126	13.9	186	4	US-09-257-825B-8
11	126	13.9	186	4	US-09-258-016-8
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19	108	11.9	191	3	US-08-655-352-5
20	108	11.9	191	4	US-08-655-352-6
21	108	11.9	191	4	US-09-258-016-5
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24	108	11.9	191	4	US-09-257-825B-6
25	106	11.7	220	4	US-09-399-913-26
26	106	11.7	220	4	US-09-298-731-26
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29	101	11.2	193	4	US-09-258-016-4	Sequence 4, Appl1
30	101	11.2	193	4	US-09-257-825B-4	Sequence 4, Appl1
31	101	11.2	220	4	US-09-399-913-24	Sequence 24, Appl1
32	101	11.2	220	4	US-09-298-731-24	Sequence 20, Appl1
33	101	11.2	222	4	US-09-399-913-20	Sequence 20, Appl1
34	101	11.2	222	4	US-09-399-913-20	Sequence 14, Appl1
35	101	11.2	270	4	US-09-399-913-14	Sequence 14, Appl1
36	101	11.2	270	4	US-09-399-913-14	Sequence 2, Appl1
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38	98	10.8	193	4	US-09-258-016-2	Sequence 18, Appl1
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40	98	10.8	270	4	US-09-298-731-18	Sequence 2, Appl1
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43	96	10.6	225	4	US-09-298-731-30	Sequence 22, Appl1
44	96	10.6	252	4	US-09-399-913-22	Sequence 28, Appl1
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ALIGNMENTS

RESULT 1
US-08-720-625-2; Sequence 2, Application US/08720625
; Patent No. 6242587

GENERAL INFORMATION:

APPLICANT: Naik, Ulhas P.

APPLICANT: Patise, Leslie V.

TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

STREET: Bell, Seltzer, Park & Gibson

CITY: Charlotte

STATE: No. 6242587th Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/08/720.625

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5470-138

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 191 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-720-625-2

Query Match	96.88;	Score 875;	DB 4;	Length 191;
Best Local Similarity	92.7%;	Pred. No. 1.9e-99;		
Matches 177;	Conservative 1;	Mismatches 13;	Indels 0;	Gaps 0;
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Db	1	MGSGSRLSKELAEYDLEFLFKOETLLAHRRCCLLPQQRVSSLAQVPEQIIS	60	
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Db 61 LPELKNPFKRICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
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Db 121 GTLNREDLSRLVNCVLGEGEDTRLSASEMKQLIDNILESDIDRGTINLSEFQHVISRS 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus

US-08-764-563-1
Query Match 96.1%; Score 869; DB 3; Length 191;
Best Local Similarity 92.1%; Pred. No. 1e-98;
Matches 176; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRRCCELLPOEQTVESSLRAQVPEQILS 60
Db 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRRCCELLPOEQXXESSLRAQVPEQILS 60

QY 61 LPELKNPFKRICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
Db 61 LPELKNPFKRICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120

QY 121 XXXXXXXXSLVNCVLGEGEDTRLSASEMKQLIDNILESDIDRGTINLSEFQHVISRS 180
Db 121 GTLNREDLSRLVNCVLGEGEDTRLSASEMKQLIDNILESDIDRGTINLSEFQHVISRS 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 3

US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 458230

US-08-764-563-3
Query Match 19.5%; Score 176.5; DB 3; Length 177;
Best Local Similarity 26.4%; Pred. No. 8.3e-14;
Matches 47; Conservative 37; Mismatches 81; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRRCCELLPOEQTVESSLRAQVPEQILS 60
Db 1 MGTNTSLRPEEVEEMOKGTNFTQKEIKKLYKRFKKLDKDGNGTISK-----DEFLM 52

QY 61 LPELKNPFKRICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
Db 53 IPELAVNPLVKRVISIFDEN-GDGSVNFKEFIAALSFNAGDKQRKLEFAFKVYDIDGD 111

QY 121 XXXXXXXXSLVNCVLGEGEDTRLSASEMKQLIDNILESDIDRGTINLSEFQHVIS 178
Db 112 GYISNGELFTVLKMWG-----NNLSDVQLAQIVDKTILEADEGDGKISFEFAKTL 165

RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322

```

1 Patent No. 5723436
2 GENERAL INFORMATION:
3 APPLICANT: Huang, Laiqiang
4 APPLICANT: Cyert, Martha S.
5 TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
6 TITLE OF INVENTION: and Methods
7 NUMBER OF SEQUENCES: 23
8 CORRESPONDENCE ADDRESSES:
9 ADDRESSEE: Dehlinger & Associates
10 STREET: 350 Cambridge Avenue, Suite 250
11 CITY: Palo Alto
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 94306
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/328,322
22 FILING DATE: 24-OCT-1994
23 CLASSIFICATION: 530
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Sholtz, Charles K.
26 REGISTRATION NUMBER: P38,615
27 REFERENCE/DOCKET NUMBER: 8600-0151.10
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (415) 324-0880
30 TELEFAX: (415) 324-0960
31 INFORMATION FOR SEQ ID NO: 17:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 174 amino acids
34 TYPE: amino acid
35 TOPOLOGY: linear
36 MOLECULE TYPE: protein
37 US-08-328-322-17
38
39 Query Match 18.2% Score 164.5, DB 1, Length 174,
40 Best Local Similarity 24.3%, Pred. No. 2, 4e-12,
41 Matches 43; Conservative 41, Mismatches 76, Indels 17, Gaps 4;
42
43 QY 1 MGGSSRSLSKELLAAYODLFTLKQELLAHRRFCELLPQEQRYWESSIRAOVPEQILS 60
44 1 MGAASRKYVDGLLED---TTFNDREIERLRKRFKMLDRDSSGSIDKN-----EFMS 48
45
46 QY 61 LPELKANPFKERICRWFSTSPAKDLSFEDFDLILSVFSPTATPDIKSHYAFRIPIKXXX 120
47 1 LPELKANPFKERICRWFSTSPAKDLSFEDFDLILSVFSPTATPDIKSHYAFRIPIKXXX 120
48
49 QY 49 IPGVSSNPLAGRIMVEFADNSGD-VDPQGFITGLSTISGSGSKREKLRFAFKYIDIDKD 107
50 108 GFISNGELFVLKIMVG---SNLDEQLQOIVPTIVENDSDGDGRISFEFKNAI 160
51
52 RESULT 5
53 US-08-328-322-15
54 Sequence 15, Application US/08328322
55 Patent No. 5723436
56 GENERAL INFORMATION:
57 APPLICANT: Huang, Laiqiang
58 APPLICANT: Cyert, Martha S.
59 TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
60 TITLE OF INVENTION: and Methods
61 NUMBER OF SEQUENCES: 23
62 CORRESPONDENCE ADDRESSES:
63 ADDRESSEE: Dehlinger & Associates
64 STREET: 350 Cambridge Avenue, Suite 250
65 CITY: Palo Alto
66 STATE: CA
67 COUNTRY: USA
68 ZIP: 94306
69 COMPUTER READABLE FORM:

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      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/328,322
        FILING DATE: 24-OCT-1994
        CLASSIFICATION: 530
      ATTORNEY/AGENT INFORMATION:
        NAME: Sholtz, Charles K.
        REGISTRATION NUMBER: P38,615
        REFERENCE/DOCKET NUMBER: 8600-0151.10
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (415) 324-0880
        TELEFAX: (415) 324-0960
      INFORMATION FOR SEQ ID NO: 15:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 157 amino acids
          TYPE: amino acid
          TOPOLOGY: linear
        MOLECULE TYPE: protein
      US-08-328-322-15

Query Match           17.0%; Score 153.5; DB 1; Length 157;
Best Local Similarity 24.0%; Pred. No. 4,6e-11;
Matches   37; Conservative    37; Mismatches   67; Indels   13; Gaps     3.

Qy      24 KOELLIAHREFCELLPQEDRTVESSIRAOVPEQLISLELANPFKERICVFSTSPAK 83
       :||::||:||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      3 ROEILRRRREKFLRDSSGSIDKN-----EFWSIRGVSNNPLAGRIIMEFDADNS 54
Qy      84 DLSFEFDLILSVSDNATPDIKSHVAERIPXXXXXXXSRVLNCLTGGEDTR 143
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      55 D-VDQERTGTGISRGSGSKDEKLRFARKIYDIDKDGFIINSGLFIYLKIWVG----SN 109
Qy      144 LSASEMKOLINDILESDIDRDGITNLSEFOHAVI 177
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      110 LDDEQLQQIVDRITYENDSDGDGRSLTFEEFNKAI 143

RESULT 6
US-08-720-625-4
; Sequence 4, Application US/08720625
; Patent No. 6242587
; GENERAL INFORMATION:
  APPLICANT: Naik, Uhas P.
  APPLICANT: Parise, Leslie V.
  TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Bell, Seltzer, Park & Gibson
    STREET: P.O. Drawer 34009
    CITY: Charlotte
    STATE: No. 6242587th Carolina
    COUNTRY: USA
    ZIP: 28234
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/720,625
    FILING DATE:
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Sidley, Kenneth D.
    REGISTRATION NUMBER: 31,665
    REFERENCE/DOCKET NUMBER: 5470-138
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 919-420-2200
    TELEFAX: 919-881-3175
  INFORMATION FOR SEQ ID NO: 4:

```


Db 71 DHEHFIYGTQSVKGEQKLRFAFRIDYMDNDGFIISNGELFOVLMKMGV-----NNLKD 126
QY 147 SEMKOLINIEESDIDRGTINLSEFOHYI 177
Db 127 WOLQOLVKSIILVLDKDGGRISPEERSDVY 157

RESULT 9
US-08-655-352-8

Sequence 8, Application US/08655352
Patent No. 6077991

GENERAL INFORMATION:

APPLICANT: Bachettira W. Poovalah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204

COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequen
DESCRIPTION: (Gen2:Profreq) with homology to 111y
DESCRIPTION: CCAMK

US-08-655-352-8

Query Match 13.9%; Score 126; DB 3; Length 186;
Best Local Similarity 22.3%; Pred. No. 1.4e-07;
Matches 44; Conservative 36; Mismatches 95; Indels 22; Gaps 5;

QY 1 MGGSGRLSKELAEYODLFTLKOELLAHRRFCELLPOEQRVYESSLRAPVPEQIIS 60
Db 1 MGRKSSRLKQDITDRITDTYFTEKEIRQMHKGFLLKDCPNGLITGEGFIKIKQF----- 55
QY 61 LPELKNPKEKICRVSTSPAKDSLSEFDELILSVESDTATPDIKSHYAFRIEXXXXX 120
Db 56 FPGDPSKRFASLVFRVDEN-NDGSIREFEIRALSVSKGL--DEKLOMARLADVND 112
QY 121 XXXXXXXXSRVYNCU-----TGEGETRLSASEMKOLINIEESDIDRGTINSE 172
Db 113 GYITREEMYNIVDAIYQWVGQOPOSEDENT-----PKRVDKIPDOMKNDKGLTLEE 166

QY 173 FOHYISRPDPASSFKI 189
Db 167 FREGSKADPRIVQALSL 183

RESULT 10
US-09-258-016-8

Sequence 8, Application US/09258016
Patent No. 6362395

GENERAL INFORMATION:

APPLICANT: Bachettira W. Poovalah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204

COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequen
DESCRIPTION: (Gen2:Profreq) with homology to 111y
DESCRIPTION: CCAMK

US-09-258-016-8

Query Match 13.9%; Score 126; DB 4; Length 186;
Best Local Similarity 22.3%; Pred. No. 1.4e-07;
Matches 44; Conservative 36; Mismatches 95; Indels 22; Gaps 5;

QY 1 MGGSGRLSKELAEYODLFTLKOELLAHRRFCELLPOEQRVYESSLRAPVPEQIIS 60
Db 1 MGRKSSRLKQDITDRITDTYFTEKEIRQMHKGFLLKDCPNGLITGEGFIKIKQF----- 55
QY 61 LPELKNPKEKICRVSTSPAKDSLSEFDELILSVESDTATPDIKSHYAFRIEXXXXX 120
Db 56 FPGDPSKRFASLVFRVDEN-NDGSIREFEIRALSVSKGL--DEKLOMARLADVND 112
QY 121 XXXXXXXXSRVYNCU-----TGEGETRLSASEMKOLINIEESDIDRGTINSE 172
Db 113 GYITREEMYNIVDAIYQWVGQOPOSEDENT-----PKRVDKIPDOMKNDKGLTLEE 166
QY 173 FOHYISRPDPASSFKI 189
Db 167 FREGSKADPRIVQALSL 183

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RESULT 11
US-09-257-825B-8
; Sequence 8, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiyah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila
US-09-257-825B-8

Query Match      13.9%; Score 126; DB 4; Length 186;
Best Local Similarity 22.3%; Pred. No. 1.4e-07;
Matches 44; Conservative 36; Mismatches 95; Indels 22; Gaps 5;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLAHRRFCELLPQQRVTVESSLRAQVPEQILS 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MGKSSKLKQDTIDRLTDTTFTTEKEIRQWHKGLKDCPNGLLTFEQGFIKIYKF----- 55
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXXX 120
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 56 FPQGPSKFAFLVRFPDEN-NDGSIFFEFIRALSVTSKGL--DEKLWAFRLYDVND 112
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 121 XXXXXXXXSRVLNCL-----TGEGDTRLASEMKQLDNLDESDDRDGTINLSE 172
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 113 GYITREMYNIVDAIYQVGOQPOSEDNT-----PQKRVYDKIFDQMKNDHDKLTLEE 166
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 173 FOHVISRSPDFASFKEI 189
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 167 FREGSKADPRIVQALS 183
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
US-08-655-352-7
; Sequence 7, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiyah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-45000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Region of rat neural visinin-like protein
; DESCRIPTION: (Gen2:Ratnvp2) with homology to lily
; DESCRIPTION: CCaMK
US-08-655-352-7

Query Match      12.9%; Score 117; DB 3; Length 191;
Best Local Similarity 22.1%; Pred. No. 1.8e-06;
Matches 45; Conservative 34; Mismatches 77; Indels 48; Gaps 5;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLAHRRFCELLPQQRVTVESSLRAQVPEQILS 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MGKNSKLAPLEEDLVQNTFESEQLKQWYKGLKDCPSGILNLEEFQQLYIKF----- 55
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXXX 120
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 56 FPYGDASKFAQHAFTFDKN-GDGTIDRFREFICALSVTS-RGSFEQKLWAFEMYD--- 109
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEM-----KQLIDNIL 157
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 110 -----LDGGRITRLEMLEIIIEAIYKMGVTVMRMNQDGLFPQQRVDKIF 155
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 158 EESDIDRDGTINLSEFQHVISRSP 181
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 156 KKMDDKDDQITLLEEFKAASDP 179
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
US-09-258-016-7
; Sequence 7, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiyah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```


NAME: Stephens Jr., Donald L.
 REGISTRATION NUMBER: 34,022
 REFERENCE/DOCKET NUMBER: 4630-51994
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 191 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: Region of rat neural visinin-like protein
 DESCRIPTION: (Gen2:Ratnvp2) with homology to 11ly
 DESCRIPTION: CCAMK
 US-09-258-016-7

Query Match 12.98; Score 117; DB 4; Length 191;
 Best Local Similarity 22.18; Pred. No. 1.8e-06;
 Matches 45; Conservative 34; Mismatches 77; Indels 48; Gaps 5;

1 MGSGSRLSKELAEYODLFLTKOEILAHRRCELLPOQRVYESSLRQVFEQILS 60
 1 MGKNSKLAEPELELDVONTFSEDELKQWTKGFLKDCPSGILNLEEFQOYIKF----- 55
 61 LPELKANPKEKICRVFTSPAKDSLSFEDELFLSVSDTATPDIKSHVAFRIKXXXX 120
 56 FPYGDASKFQAHAFRTDKN-GDGTIDREFICALSVTS-RGSFQKLNWAFEMD----- 109
 121 XXXXXXXXSRVNLCTGEGEDTRLASSEM-----KOLIDNLT 157
 110 -----LDGDGRITRLEMLEIETAIYKMGVTIMMRNODGLPQQRVDKIF 155
 158 EESDIDRDGTINLSEFOHVISRSP 181
 156 KKMDDQKDDQITLSEFKEAKSDP 179

RESULT 14

US-09-257-825B-7
 Sequence 7, Application US/09257825B
 Patent No. 6403352
 GENERAL INFORMATION:
 APPLICANT: Poovalah, Bachettira W.
 APPLICANT: Patil, Shameekumar
 APPLICANT: Takezawa, Daisuke
 TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
 FILE REFERENCE: 4630-51993
 CURRENT APPLICATION NUMBER: US/09/257,825B
 CURRENT FILING DATE: 1999-02-25
 PRIOR APPLICATION NUMBER: US 08/655,352
 PRIOR FILING DATE: 1996-05-23
 PRIOR APPLICATION NUMBER: US 60/014,743
 PRIOR FILING DATE: 1996-03-28
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 7
 LENGTH: 191
 TYPE: PRT
 ORGANISM: Rat
 US-09-257-825B-7

Query Match 12.98; Score 117; DB 4; Length 191;
 Best Local Similarity 22.18; Pred. No. 1.8e-06;
 Matches 45; Conservative 34; Mismatches 77; Indels 48; Gaps 5;

1 MGSGSRLSKELAEYODLFLTKOEILAHRRCELLPOQRVYESSLRQVFEQILS 60
 1 MGKNSKLAEPELELDVONTFSEDELKQWTKGFLKDCPSGILNLEEFQOYIKF----- 55
 61 LPELKANPKEKICRVFTSPAKDSLSFEDELFLSVSDTATPDIKSHVAFRIKXXXX 120
 56 FPYGDASKFQAHAFRTDKN-GDGTIDREFICALSVTS-RGSFQKLNWAFEMD----- 109

121 XXXXXXXXSRVNLCTGEGEDTRLASEM-----KOLIDNLT 157
 110 -----LDGDGRITRLEMLEIETAIYKMGVTIMMRNODGLPQQRVDKIF 155
 158 EESDIDRDGTINLSEFOHVISRSP 181
 156 KKMDDQKDDQITLSEFKEAKSDP 179

RESULT 15

US-08-655-352-3
 Sequence 3, Application US/08655352
 Patent No. 6077991
 GENERAL INFORMATION:
 APPLICANT: Bachettira W. Poovalah, Zhilua Liu,
 APPLICANT: Shameekumar Patil, Daisuke Takezawa
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klargust Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/655,352
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/323,449
 FILING DATE: October 14, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-45000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: Region of rat neural visinin-like protein
 DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
 DESCRIPTION: CCAMK
 US-08-655-352-3

Query Match 12.88; Score 116; DB 3; Length 193;
 Best Local Similarity 22.48; Pred. No. 2.5e-06;
 Matches 50; Conservative 35; Mismatches 72; Indels 66; Gaps 8;

1 MGSGSRLSKELAEYODLFLTKOEILAHRRCELLPOQRVYESSLRQVFEQILS 60
 1 MGKNSKLAEPELELDVONTFSEDELKQWTKGFLKDCPSGILNLEEFQOYIKF-----FKRIVA 53
 61 --LPELKANPKEKICRVFTSPAKDSLSFEDELFLSVSDTATPDIKSHVAFRIKXXX 118
 54 NFPPYGDASKFAEHVFRFDIN-SDGTIDREFICALSVTS-RKLEQKLNWAFEMD-- 109
 119 XXXXXXXXSRVNLCTGEGEDTRLASEMKOLI-----D 154

Db 110 -----LDGNG---YISRSEMLEIVQAIYKMVSSYMKMPEDESTPEKRTD 150
QY 155 NILESDIDRDGTINLSEF-----QHVISRSPDPFASF 187
Db 151 KIFRQMDINNDGKLSLEEFKGAKSDPSIVRLQCDPSSASQF 193

Search completed: January 17, 2003, 12:47:13
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:45:39 : Search time 11 Seconds
(without alignments)
345.163 Million cell updates/sec

Title: US-09-878-454A-2X
Perfect score: 904
Sequence: 1 MGSGLSKELLARYODLT.....EFQHVISRSPDFASSRKIVL 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_AA:
1: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata1/pubpaa/PCURS_PUBCOMB.pep.*
8: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
10: /cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	97.2	191	10	US-09-878-454A-2
2	867	95.9	191	12	US-10-109-885-2
3	309	34.2	187	10	US-09-802-116-2
4	146.5	16.2	170	12	US-10-109-885-3
5	136.5	15.1	195	10	US-09-999-602-3
6	132.5	14.7	195	10	US-09-999-602-4
7	130	14.4	214	10	US-09-999-602-1
8	106	11.7	220	10	US-09-874-26
9	101	11.2	220	10	US-09-350-874-24
10	101	11.2	252	10	US-09-350-874-20
11	101	11.2	270	10	US-09-350-874-14
12	98	10.8	225	10	US-09-350-874-18
13	96	10.6	225	10	US-09-350-874-30
14	96	10.6	252	10	US-09-350-874-22
15	96	10.6	252	10	US-09-350-874-28
16	96	10.6	252	10	US-09-350-874-42
17	96	10.6	257	10	US-09-350-874-16
18	90	10.0	216	10	US-09-350-874-6
19	90	10.0	227	10	US-09-350-874-8

20	90	10.0	227	10	US-09-350-874-10	Sequence 10, Appl
21	89	9.8	245	10	US-09-350-874-4	Sequence 4, Appl1
22	89	9.8	216	9	US-09-965-528-15	Sequence 15, Appl
23	89	9.8	142	10	US-09-350-874-2	Sequence 2, Appl1
24	85.5	9.5	142	10	US-09-910-071-4	Sequence 4, Appl1
25	85	9.4	642	9	US-09-554-000-6	Sequence 6, Appl1
26	85	9.4	656	9	US-09-554-000-8	Sequence 8, Appl1
27	84	9.3	642	9	US-09-554-000-2	Sequence 2, Appl1
28	84	9.3	652	9	US-09-554-000-4	Sequence 4, Appl1
29	82	9.1	229	10	US-09-350-874-70	Sequence 70, Appl
30	82	9.1	233	10	US-09-350-874-49	Sequence 49, Appl
31	82	9.1	250	10	US-09-350-874-72	Sequence 72, Appl
32	80.5	8.9	172	12	US-10-109-885-4	Sequence 4, Appl1
33	79.5	8.8	139	10	US-09-864-761-34808	Sequence 34808, A
34	74	8.2	256	10	US-09-350-874-36	Sequence 36, Appl
35	72.5	8.0	159	10	US-09-910-071-5	Sequence 5, Appl1
36	71.5	7.9	1230	9	US-10-025-380-692	Sequence 692, App
37	71.5	7.9	1210	10	US-09-922-217-692	Sequence 692, App
38	71.5	7.9	1210	10	US-09-833-263-692	Sequence 692, App
39	71.5	7.9	1548	10	US-10-025-380-1095	Sequence 1095, Ap
40	71.5	7.9	1548	10	US-09-922-217-1095	Sequence 1095, Ap
41	71	7.9	203	10	US-09-350-874-12	Sequence 12, Appl
42	71	7.9	256	10	US-09-826-589-3	Sequence 32, Appl
43	70.5	7.8	90	10	US-09-826-589-4	Sequence 3, Appl1
44	70.5	7.8	90	10	US-09-826-589-4	Sequence 4, Appl1
45	70.5	7.8	90	10	US-09-872-185B-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montelito, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
PRIORITY FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match 97.2% Score 879; DB 10; Length 191;
Best Local Similarity 93.2% Pred. No. 2e-92;
Matches 178; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 MGSGLSKELLARYODLTFTYKOEILLAHRFCELLPOEORTVESSLRAOPEOILS 60
DB 1 MGSGLSKELLARYODLTFTYKOEILLAHRFCELLPOEORTVESSLRAOPEOILS 60
QY 61 LPELANPFEKICVFTSTSPAKDSLSEDFELLIVSVSDATPDIKSHVAFRIYXXXX 120
DB 61 LPELANPFEKICVFTSTSPAKDSLSEDFELLIVSVSDATPDIKSHVAFRIYXXXX 120
QY 121 XXXXXXXXSRILVNCITGSGEDTRLSASBMKOLINILLESIDRGTINLSEFOHVSRS 180
DB 121 GTLNEDLSRLVNCITGSGEDTRLSASBMKOLINILLESIDRGTINLSEFOHVSRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 2

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US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; FILE REFERENCE: REVEL-14A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/10/109,885
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match      95.9%; Score 867; DB 12; Length 191;
Best Local Similarity 92.1%; Pred. No. 4.7e-91;
Matches 176; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGGSGRLSKELLAAYQDLTLTKQETLLAHRRCCELLPOQRVSSESLRAQVPEQLLS 60
DB 1 MGGSGRLSKELLAAYQDLTLTKQETLLAHRRCCELLPOQRVSSESLRAQVPEQLLS 60
QY 61 LPELKANPKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
DB 61 LPELKANPKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
QY 121 XXXXXXXXSRVLNCLTGEDETRLSASEMKQLIDNILEESDIDRGTINLSEFQHV 180
DB 121 GTLNREDLSRLVNLCTGEDETRLSASEMKQLIDYILEESDIDRGTINLSEFQHV 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020082406A1el Human Kinase Interacting Protein and Polyno
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match      34.2%; Score 309; DB 10; Length 187;
Best Local Similarity 37.8%; Pred. No. 1e-27; Indels 12; Gaps 5;
Matches 73; Conservative 39; Mismatches 69; Indels 12; Gaps 5;

US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; FILE REFERENCE: REVEL-14A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/10/109,885
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match      16.2%; Score 146.5; DB 12; Length 170;
Best Local Similarity 27.0%; Pred. No. 2.5e-09;
Matches 33; Conservative 29; Mismatches 55; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRI 115
DB 41 EEFMSLPELQONPLVQRVIDIFDTD-GNGEVDKFKEGVSQFVKGQKQELRFAFR 99
QY 116 XXXXXXXXSRVLNCLTGEDETRLSASEMKQLIDNILEESDIDRGTINLSEFQHV 175
DB 100 DMKDGYISNGELFQVLKMMVG----NNLKDTQLQIVDKTTINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
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;; CURRENT APPLICATION NUMBER: US/09/999,602
;; CURRENT FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 09/010,378
;; PRIOR FILING DATE: 1998-01-21
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PERL Program
;; SEQ ID NO 3
;; LENGTH: 195
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1226242
US-09-999-602-3
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Query Match 15.18% Score 136.5; DB 10; Length 195;
Best Local Similarity 24.18; Pred. No. 4.1e-08;
Matches 47; Conservative 32; Mismatches 87; Indels 29; Gaps 6;
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QY 1 MGSQSGSRISK-ELLAETODLFTLKQELLAHRRFCCLLPQEQRTVESSLRAQVPEQL 59
DB 1 MGSRASTLRLDELELEIKETGFSHQIRLYSRFTSLDKGNGTLSR-----EDFQ 52
QY 60 SLPELKANPFKERICRVSTSPAKDSLSPEDFLDLVSF-----SDTATPD----- 105
DB 53 RIPELAINPLGRITIAF-FSEGEDQVNRGFMRTLAHFRPIEDNKSMDVNGPEPLNSR 111
QY 106 -IKSHVAFRIEYXXXXXXXSRVNLCTGEGEDTRLASSEMQLDINILEESDIDR 164
DB 112 SNKLFARFLYLDKDKISRDLELLQVLRMVG-----VNISDQLSIADRTIOEADQDG 167
QY 165 DGTINLSEFOHVISR 179
DB 168 DSAISFTFEVKVLEK 182
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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT FILING DATE: 2001-10-25
; CURRENT APPLICATION NUMBER: US/09/999,602
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1706967
US-09-999-602-4
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Query Match 14.7%; Score 132.5; DB 10; Length 195;
Best Local Similarity 23.68; Pred. No. 1.2e-07;
Matches 46; Conservative 32; Mismatches 88; Indels 29; Gaps 6;
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QY 1 MGSQSGSRISK-ELLAETODLFTLKQELLAHRRFCCLLPQEQRTVESSLRAQVPEQL 59
DB 1 MGSRASTLRLDELELEIKETGFSHQIRLYSRFTSLDKGNGTLSR-----EDFQ 52
QY 60 SLPELKANPFKERICRVSTSPAKDSLSPEDFLDLVSF-----SDTATPD----- 105
DB 53 RIPELAINPLGRITIAF-FSEGEDQVNRGFMRTLAHFRPIEDNKSMDVNGPEPLNSR 111
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QY 106 -IKSHVAFRIEYXXXXXXXXXXSRVNLCTGEGEDTRLASSEMQLDINILEESDIDR 164
DB 112 SNKLFARFLYLDKDKISRDLELLQVLRMVG-----VNISDQLSIADRTIOEADQDG 167
QY 165 DGTINLSEFOHVISR 179
DB 168 DSAISFTFEVKVLEK 182
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RESULT 7
US-09-999-602-1
; Sequence 1, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 134682
US-09-999-602-1
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Query Match 14.4%; Score 130; DB 10; Length 214;
Best Local Similarity 24.38; Pred. No. 2.6e-07;
Matches 45; Conservative 28; Mismatches 58; Indels 54; Gaps 6;
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QY 1 MGSQSGSRISKELLAETODLFTLKQELLAHRRFCCLLPQEQRTVESSLRAQVPEQL 60
DB 1 MGAHNS--ASEYVRELEGTGFSQDIEQLHRRF-KOLSGDDPTIRK-----ENFYN 49
QY 61 LPELKANPFKERICRVF-----STSPAKDSLSPEDFLDLVSFSDTATPDIKSHVAF 112
DB 50 VPDLEINPLRSIVRAFFDNRLKPGSLADEINFEDELITMSYFRPIDT----- 100
QY 113 RIFXXXXXXXSRVNLCTGEGEDTRLASSEMQLDINILEESDIDBDGTINLSE 172
DB 101 -----TMDERQVELSRKREKLFLEFHMV-----DSQSDGRITILEE 134
QY 173 FQHV 177
DB 135 YRNV 139
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RESULT 8
US-09-350-874-26
; Sequence 26, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MN1-069
; CURRENT FILING DATE: 1999-07-09
; CURRENT APPLICATION NUMBER: US/09/350,874
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
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; NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 270
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-350-874-18

Query Match 11.2% Score 101; DB 10; Length 270;
 Best Local Similarity 21.4%; Pred. No. 0.0007;
 Matches 42; Conservative 40; Mismatches 76; Indels 38; Gaps 7;

QY 11 ELAAYODLFLTKOEILLARRECELLPOORFVSSSLRAOVPEQILS--LPELKAMP 68
 DB 91 EGLELOEQOTFKTRRELQVLYRGFKNECP-----SGIVNEENKQIYSQFFQGDSSN 143
 QY 69 FKERICRVSTSPAKDSISFEDFLDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 144 YATFLFNAFDTN-HDGSVFEDFVAGLSVIL-RGIVDDRLMNAFNLVDLND----- 193
 QY 129 SRLVNCITGE-----GEDT--RLSASEMKOLINILEESDIDRGTINLSEF 173
 DB 194 -----GCITKEMLDIMKSIYDMGKYTYPALREAPREHVESFQKDRNDGVVITIEEF 249
 QY 174 QHVISRSPDFASSEFKI 189
 DB 250 IESQKDEINIRSMQL 265

RESULT 12
 US-09-350-874-18
 Sequence 18, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wenqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: NMI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER FILING DATE: 1998-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 18
 LENGTH: 270
 TYPE: PRF
 ORGANISM: Mus musculus
 US-09-350-874-18

Query Match 10.8% Score 98; DB 10; Length 270;
 Best Local Similarity 22.8%; Pred. No. 0.0015;
 Matches 41; Conservative 36; Mismatches 65; Indels 38; Gaps 7;

QY 11 ELAAYODLFLTKOEILLARRECELLPOORFVSSSLRAOVPEQILS--LPELKAMP 68
 DB 91 EGLELOEQOTFKTRRELQVLYRGFKNECP-----SGIVNEENKQIYSQFFQGDSSN 143
 QY 69 FKERICRVSTSPAKDSISFEDFLDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 144 YATFLFNAFDTN-HDGSVFEDFVAGLSVIL-RGIVDDRLMNAFNLVDLND----- 193
 QY 129 SRLVNCITGE-----GEDT--RLSASEMKOLINILEESDIDRGTINLSEF 173
 DB 194 -----GCITKEMLDIMKSIYDMGKYTYPALREAPREHVESFQKDRNDGVVITIEEF 249

RESULT 13

US-09-350-874-30
 Sequence 30, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wenqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: NMI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 30
 LENGTH: 225
 TYPE: PRF
 ORGANISM: Rattus sp.
 US-09-350-874-30

Query Match 10.6% Score 96; DB 10; Length 225;
 Best Local Similarity 22.8%; Pred. No. 0.002;
 Matches 41; Conservative 35; Mismatches 66; Indels 38; Gaps 7;

QY 11 ELAAYODLFLTKOEILLARRECELLPOORFVSSSLRAOVPEQILS--LPELKAMP 68
 DB 46 EGLELOEQOTFKTRRELQVLYRGFKNECP-----SGIVNEENKQIYSQFFQGDSSN 98
 QY 69 FKERICRVSTSPAKDSISFEDFLDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 99 YATFLFNAFDTN-HDGSVFEDFVAGLSVIL-RGIVDDRLMNAFNLVDLND----- 148
 QY 129 SRLVNCITGE-----GEDT--RLSASEMKOLINILEESDIDRGTINLSEF 173
 DB 149 -----GCITKEMLDIMKSIYDMGKYTYPALREAPREHVESFQKDRNDGVVITIEEF 204

RESULT 14
 US-09-350-874-22
 Sequence 22, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wenqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: NMI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 252
 TYPE: PRF
 ORGANISM: Rattus sp.
 US-09-350-874-22

Query Match 10.6% Score 96; DB 10; Length 252;
 Best Local Similarity 22.8%; Pred. No. 0.0024;
 Matches 41; Conservative 35; Mismatches 66; Indels 38; Gaps 7;

Search completed: January 17, 2003, 12:47:31
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:44:38 ; Search time 17 seconds
(without alignments)
1080.099 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MGSGSGSRLSKELAEYODLT.....EFQHVYSRSPDFASFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	367	40.6	311.2	T21563 hypothetical prote
2	171.5	19.0	174.2	T41632 probable calcineur
3	164.5	18.2	175.2	JH0462 phosphoprotein pho
4	160.5	17.8	174.2	T47245 calcineurin regula
5	146.5	16.2	170.1	A33391 calcineurin regula
6	146.5	16.2	170.1	A34137 calcineurin regula
7	146.5	16.2	170.1	JC1230 calcineurin regula
8	146.5	16.2	216.1	S42716 calcineurin regula
9	144.5	16.0	369.2	T22708 calcineurin regula
10	140.5	15.5	195.2	T28047 hypothetical prote
11	139.5	15.4	213.2	T31775 hypothetical prote
12	136.5	15.1	170.2	JC5174 calcineurin regula
13	135.5	15.0	170.2	JC7242 calcineurin regula
14	132.5	14.7	170.2	A44307 calcineurin regula
15	130.5	14.4	179.2	JC1221 calcineurin regula
16	130.5	14.4	226.2	T51357 calcineurin B-like
17	128.5	14.2	165.2	PS0261 calcineurin regula
18	128.5	14.2	176.2	JC1232 calcineurin regula
19	123.5	13.7	190.2	T20725 calcineurin regula
20	121	13.4	192.2	T01375 calcineurin regula
21	118.5	13.1	226.2	T08923 calcium sensor hom
22	117	12.9	193.2	JH0815 calcineurin B-like
23	117	12.9	193.2	JH0815 calcineurin B-like
24	117	12.9	246.2	T05308 neuronal visinin-lik
25	117	12.9	246.2	H85387 hypothetical prote
26	116	12.8	193.2	T50676 gene Rem-1 protein
27	116	12.8	193.2	S47365 calcium-binding pr
28	114.5	12.7	213.2	T51356 calcineurin B-like
29	114	12.6	190.2	T51686 frequenin - Africa

30	111	12.3	224.2	F96658 protein F96658
31	108	11.9	191.2	JH0605 neuronal visinin-lik
32	108	11.9	191.2	A48979 visinin-lik prote
33	106	11.7	190.2	A55666 neurocalcin - fruit
34	102	11.3	193.2	JH0616 neurocalcin (clone
35	101	11.2	270.2	JC7631 K+ channel-interac
36	99	11.0	190.2	S61168 hypothetical prote
37	98.5	10.9	172.2	S38531 caltractin - mouse
38	97	10.7	165.2	A44103 neurocalcin beta -
39	97	10.7	193.2	JC2186 hippocalcin - huma
40	96.5	10.7	155.2	S38877 calmodulin 8 (limp
41	96	10.6	151.2	A71409 related to neuroma
42	96	10.6	190.2	S58303 centrin - human
43	95.5	10.6	172.2	I38424 tropoin C-1 - gila
44	94.5	10.5	158.2	A38397 calcium-dependent
45	94.5	10.5	571.2	T00835

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19442
A:Accession: T21563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-311 <WILD>
A:Molecule type: DNA
A:Cross-references: EMBL:Z81072; PIDN: CAB03019.1; GSPDB: GN00019; CESP: F30A10.1
A:Experimental source: clone F30A10
C:Genetics:
A:Gene: CESP:F30A10.1
A:Map position: 1
A:Introns: 106/2; 139/3; 190/3; 240/1

Query Match Best Local Similarity 40.6%; Score 367; DB 2; Length 311;
Matches 82; Conservative 39; Mismatches 60; Indels 26; Gaps 5;

QY 1 MGSGSGSRLS-----KELAEYODLFLFKOETLLAHRRCCELLPQEQRTYESS 48
DB 111 MGNMSSLSLELNFSGKGVFTREODCTFTTKDILRLKRYALNPHK--VPTN 167
QY 49 LRAQVP-----FEQILSPLEKAMPFKERICRVSTSPAKDSLSEDFLDLSVSDPA 102
DB 168 MGNRPATITLFEFEVEKKEPELKENPFRIRIEVS-EDGRNLTSDPDLDFSVSEMA 226
QY 103 TPDISHVAFRFXKXXXXXXXXXXSRVLCVTEGEGEDFLASAEKQLDNIIEESDI 162
DB 227 PLQIKRYAFRIYDGDDELGHDLCKMIRSLTRD---ELSDVEVERIIRIIEEDL 282
QY 163 DRDGTINLSEFOHVSRSRSPDFASFKI 189
DB 283 DEDSSINFAEFHVSRSRSPDFIRTFHI 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C:Accession: T41632
R:McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z22005
A:Accession: T41632
A:Status: preliminary; translated from GB/EMBL/DBJ

[illegible]

A: Experimental source: brain
C: Comment: With calcineurin catalytic chain plays an important role in neural and nonneural
C: Genetics:

A: Gene: PP2B-beta-1
A: Complex: heterodimer with calcineurin catalytic chain
C: Superfamily: calmodulin; calmodulin repeat homology
C: Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipid
F: 2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F: 18-49/Domain: calmodulin repeat homology <EF1>
F: 50-82/Domain: calmodulin repeat homology <EF2>
F: 87-119/Domain: calmodulin repeat homology <EF3>
F: 128-160/Domain: calmodulin repeat homology <EF4>
F: 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 16.2%; Score 146.5; DB 1; Length 170;
Best Local Similarity 27.0%; Pred. No. 3.2e-06;
Matches 33; Conservative 29; Mismatches 55; Indels 5; Gaps 2;

Qy 56 EOILSLPELKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAPRIF 115

Db 41 EEFNSLPELQONPLVQRVIDIFDTD-GNGEVDFFKEFIEGVSVQSGDKGKQLRFAFRIF 99

Qy 116 XXXXXXXXXXXXXSRVNCVLTGEGEDTRLSASEMKQLIDNLEESDIDRDGTINLSEFOH 175

Db 100 DMDXGYSINGELFQVLKMMVG-----NNLKDTQLQIVDKTIINADKDGGRISFEFCA 155

Qy 176 VI 177

Db 156 VV 157

RESULT 8

S42716
calcineurin regulatory chain, long splice form - rat
N: Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
N: Contains: calcineurin regulatory chain, short splice form
C: Species: Rattus norvegicus (Norway rat)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C: Accession: S42716; S42717
R: Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
Biochim. Biophys. Acta 1217, 174-180, 1994
A: Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of calcineurin
A: Reference number: S42716; MUID: 94153993; PMID: 8110831
A: Accession: S42716

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-216 <CHAL>

A: Cross-references: EMBL:D14425; NID: g286205; PIDN: BAA03318.1; PID: g286206

A: Accession: S42717

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 'M', 48-216 <CHAZ>

A: Cross-references: EMBL:D14568; NID: g286255; PIDN: BAA03422.1; PID: g286256

A: Complex: heterodimer with calcineurin catalytic chain

C: Superfamily: calmodulin; calmodulin repeat homology

C: Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF hand

F: 2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MAT>

F: 48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MAT>

F: 64-95/Domain: calmodulin repeat homology <EF1>

F: 96-128/Domain: calmodulin repeat homology <EF2>

F: 'M', 48-216/Product: calcineurin regulatory chain, short splice form precursor #status

F: 133-165/Domain: calmodulin repeat homology <EF3>

F: 174-206/Domain: calmodulin repeat homology <EF4>

F: 48/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

F: 49/Modified site: aspartic acid (Asn) #status predicted

Query Match 16.2%; Score 146.5; DB 1; Length 216;

Best Local Similarity 27.0%; Pred. No. 4.2e-06;

Matches 33; Conservative 29; Mismatches 55; Indels 5; Gaps 2;

Qy 56 EOILSLPELKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAPRIF 115

Db 87 EEFNSLPELQONPLVQRVIDIFDTD-GNGEVDFFKEFIEGVSVQSGDKGKQLRFAFRIF 145

Qy 116 XXXXXXXXXXXXXSRVNCVLTGEGEDTRLSASEMKQLIDNLEESDIDRDGTINLSEFOH 175

Db 146 DMDXGYSINGELFQVLKMMVG-----NNLKDTQLQIVDKTIINADKDGGRISFEFCA 201

Qy 176 VI 177

Db 202 VV 203

RESULT 9

T22708

hypothetical protein F55C10.1 - Caenorhabditis elegans

C: Species: Caenorhabditis elegans

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C: Accession: T22708

R: Dobson, R.

submitted to the EMBL Data Library, June 1996

A: Reference number: Z19603

A: Accession: T22708

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-369 <WIL>

A: Cross-references: EMBL: Z74036; PIDN: CAA94849.1; GSPDB: GN00023; CESP: F55C10.1

A: Experimental source: clone F55C10

C: Genetics:

A: Gene: CESP: F55C10.1

A: Map position: 5

A: Introns: 159/2; 199/3; 213/1; 272/1; 312/3; 353/3

Query Match 16.0%; Score 144.5; DB 2; Length 369;

Best Local Similarity 25.0%; Pred. No. 1.2e-05;

Matches 45; Conservative 35; Mismatches 77; Indels 23; Gaps 6;

Qy 3 GSGSRLSKELLAEXQ--DLTFLTKQEIILAHRRFCELLPQEQRTVESLRAQVPEQILS 60

Db 200 GADASLPMEMCNFNDAYELRLT-----RRPKKL-----DVDGS--GSLSVVEEFMS 243

Qy 61 LPEKANPFKRICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAPRIFXXXX 120

Db 244 LPELQONPLVQRVIDIFD-EDNGEVDFFKEFIEGVSVQSGDKGKQLRFAFRIFDMDRD 302

Qy 121 XXXXXXXXXXXXXSRVNCVLTGEGEDTRLSASEMKQLIDNLEESDIDRDGTINLSEFOHVISR 180

Db 303 GFISNGELFQVLKMMVG-----NNLKDSQLQIVDKTIILFHKDGGKISFQEFCDVHT 358

RESULT 10

T28047

hypothetical protein ZK856.8 - Caenorhabditis elegans

C: Species: Caenorhabditis elegans

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C: Accession: T28047

R: Lloyd, C.

submitted to the EMBL Data Library, April 1996

A: Reference number: Z20461

A: Accession: T28047

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-195 <WIL>

A: Cross-references: EMBL: Z70783; PIDN: CAA94856.1; GSPDB: GN00023; CESP: ZK856.8

A: Experimental source: clone ZK856

C: Genetics:

A: Gene: CESP: ZK856.8

A: Map position: 5

A: Introns: 23/1; 42/1; 117/1

Query Match 15.5%; Score 140.5; DB 2; Length 195;

Best Local Similarity 22.3%; Pred. No. 1.3e-05;

Matches 44; Conservative 40; Mismatches 82; Indels 31; Gaps 6;

Qy 1 MGGSGS-RLSKELLAEXQDLTFLTKQEIILAHRRFCELLPQEQRTVESLRAQVPEQIL 59

Db 1 MGGSGS-RLSKELLAEXQDLTFLTKQEIILAHRRFCELLPQEQRTVESLRAQVPEQIL 59

Db 1 MGSSSLMLRDEEEETERNNOIVRLYRFLSLDKKGQGLSR-----DDEL 52
 QY 60 SLPELAMPKERICRVFSTSPA-----KDSLSFEDFLDLVSFSDTATPDIKSH---- 109
 Db 53 NPELAVNPLGDRIVDAFFLASSNGDNEQOLNFRQVAILAHFOISR--YKKNALNS 110
 QY 110 -----YARIFXXXXXXXSRVNCCLTGEEDTRLASSEMQLIDNILEESDID 163
 Db 111 RKDKLLFAFKMYDLNKNNDYTRREEFYILNSMVG-----ANITSDQLDKINDRTLEADAD 166
 QY 164 RQGTINLSEFOHVISRS 180
 Db 167 RQGISFDEFRCAMEXT 183

RESULT 11
 131775
 hypothetical protein F59D6.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31775
 R:Bradshaw, H.; Graves, T.
 Submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F59D6.
 A:Reference number: 221083
 A:Accession: T31775
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-213 <BRA>
 A:Cross-references: EMBL:AF016435; PIDN:AAB65882.1; GSPDB:GN00023; CESP:F59D6.7
 A:Experimental source: strain Bristol N2; clone F59D6
 C:Genetics:
 A:Gene: CESP:F59D6.7
 A:Map position: 5
 A:Introns: 24/2; 60/1; 135/1

Query Match 15.4%; Score 139.5; DB 2; Length 213;
 Best Local Similarity 22.1%; Pred. No. 1.8e-05;
 Matches 47; Conservative 40; Mismatches 81; Indels 45; Gaps 7;

QY 1 MGSSSRL-----SKELLAEO-----DLFLTKOETILAHRRFCLELPOE 41
 Db 1 MGNSSSLSLDAEMREIMDEPOCKVCYIIAKQFTPKNTISVKNHQLRLYTRFASL---- 56
 QY 42 QRTVSSSLRAQYPEOILSLPELAMPKERICRVFSTSPAND-----SLSEDFDL 95
 Db 57 -----DKNGGYLSRDFLNPVELAVNPLGDRILDAFTLGDSDGSKSQTLFRQGVRL 112
 QY 96 SVF-----SDTAPDIKS--HYAFRIFXXXXXXXSRVNCCLTGEEDTRLAS 147
 Db 113 AHFOPIKVKDNALNSRKDLRFKFKMYDLNKNNTYTRREEFYILNSMVG-----ANITSD 168
 QY 148 EMKQIDNILEESDIDRGTINLSEFOHVISRS 180
 Db 169 QLDKIDKTLLEADQDRGKISFDEFRCAMEXT 201

RESULT 12
 JC5174
 calcineurin regulatory chain 2 - fruit fly (*Drosophila melanogaster*)
 N:Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein phosph
 C:Species: *Drosophila melanogaster*
 C:Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
 C:Accession: JC5174
 R:Marren, W.D.; Phillips, A.M.; Howells, A.J.
 Gene 177, 149-153, 1996
 A:Title: *Drosophila melanogaster* contains both X-linked and autosomal homologues of the
 A:Reference number: JC5174; MUID:97080515; PMID:8921860
 A:Accession: JC5174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-170 <VAR>
 A:Cross-references: GB:U56245; NID:g1336009; PIDN:AA047350.1; PID:g1336010

C:Comment: This protein is the calcium binding chain of calcineurin, involved in C
 C:Genetics:
 A:Gene: dcmb2
 C:Complex: heterodimer with calcineurin catalytic chain
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
 F/2-170/Product: calcineurin regulatory chain (status predicted <MAY>
 F/18-49/Domain: calmodulin repeat homology <EF1>
 F/87-119/Domain: calmodulin repeat homology <EF2>
 F/128-160/Domain: calmodulin repeat homology <EF3>
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/3/Modified site: aspartic acid (Asn) #status predicted

Query Match 15.1%; Score 136.5; DB 2; Length 170;
 Best Local Similarity 21.9%; Pred. No. 2.6e-05;
 Matches 39; Conservative 39; Mismatches 81; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAEYQDLFTKQETILAHRRFCLELPOEORTVSSSLRAQVPEOILSLP 62
 Db 2 GNELSLPEMLCSNFD-----ADEIRRLGRF-----RKLDLNSGALSDERMSLP 47
 QY 63 ELKANPFEKRICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIKXXXXXX 122
 Db 48 ELQGNPLVQRYDIDFD-ADNGEVDFKEFIQGVSVKGDKSLRFRFRIYDMNDGX 106
 QY 123 XXXXXXSRVNCCLTGEEDTRLASSEMQLIDNILEESDIDRGTINLSEFOHVISRS 180
 Db 107 ISNGELFQVLKMMVG-----NNLKDTQLQIVDKTIOFADKDEGKISFDEFCSVANT 160

RESULT 13
 JC7242
 calcineurin regulatory subunit, calcineurin B - scallop (*Patinopecten yessoensis*)
 N:Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory
 C:Species: *Patinopecten yessoensis* (Yesso scallop)
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C:Accession: JC7242; PC7070
 R:Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatsuse, R.; Yazawa, M.
 J. Biochem. 127, 739-746, 2000
 A:Title: Molecular cloning of cDNA encoding two subunits of calcineurin from scallop
 A:Reference number: JC7241
 A:Accession: JC7242
 A:Molecule type: mRNA
 A:Residues: 1-170 <URX>
 A:Cross-references: DDBJ:AB041524
 A:Experimental source: testis
 A:Accession: PC7070
 A:Molecule type: protein
 A:Residues: 12-68;73-85;92-170 <UR2>
 C:Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-spec.
 C:Genetics:
 A:Gene: cnb
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; flagellar rotation; myristylation; phosphop

Query Match 15.0%; Score 135.5; DB 2; Length 170;
 Best Local Similarity 22.3%; Pred. No. 3.2e-05;
 Matches 39; Conservative 38; Mismatches 79; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAEYQDLFTKQETILAHRRFCLELPOEORTVSSSLRAQVPEOILSLP 62
 Db 2 GNELSLPEMLCSNFD-----PDEIRRLGRF-----RKLDLNSGALSDERMFLP 47
 QY 63 ELKANPFEKRICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIKXXXXXX 122
 Db 48 ELQGNPLVQRYDIDFD-ADNGEVDFKEFIQGVSVKGDKSLRFRFRIYDMNDGX 106
 QY 123 XXXXXXSRVNCCLTGEEDTRLASSEMQLIDNILEESDIDRGTINLSEFOHVISRS 177
 Db 107 ISNGELFQVLKMMVG-----NNLKDTQLQIVDKTIIHADADGDKISFEFCAYV 157

RESULT 14

A44307
calcineurin regulatory chain 1 - fruit fly (Drosophila melanogaster)
N:Alternate names: calcineurin beta subunit; calcineurin chain B-1; phosphoprotein phosph
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A44307
R:Guerini, D.; Montell, C.; Klee, C.B.
J. Biol. Chem. 267, 22542-22549, 1992
A:Title: Molecular cloning and characterization of the genes encoding the two subunits of
A:Reference number: A44307; MUID:93054551; PMID:1331060
A:Accession: A44307
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
A:Note: sequence extracted from NCBI backbone (NCBIP:117113)
C:Genetics:
A:Gene: FlyBase:CanB
A:Cross-references: FlyBase:FBgn0010014
A:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 14.7%; Score 132.5; DB 2; Length 170;
Best Local Similarity 23.2%; Pred. No. 6.1e-05;
Matches 36; Conservative 34; Mismatches 72; Indels 13; Gaps 3;

QY 26 EILLHRRFCLELPQEQRTVESLRQVPEQILSLPELKANPFKERICRVFSTSPAKDS 85

Db 19 EIRLGRKF-----RKLDNSGALSIDFMSLPQLQONPLVQRVIDIFD-ADNGE 69

QY 86 LSPEDFDLLSVFSDTATPKIKSHYAFRIFFXXXXXXXSRVLNCLTGEGETRLS 145

Db 70 VDFKEFTQGVSVRGDKSLKLFAPRIYDMNDGFIISNGELFQVLKMMVG----NNLK 125

QY 146 ASEMQLIDNILESDIDRDGTINLSEFQHVIRS 180

Db 126 DTQLQIVDKTICFADKDEGDKISDFEFCVVGNT 160

RESULT 15

JC1221
calcineurin regulatory chain, testis - mouse
N:Alternate names: calcineurin beta-2 subunit; calcineurin chain B-2; phosphoprotein pho
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: JC1221
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A:Title: Structure and expression of two isoforms of the murine calmodulin-dependent pro
A:Reference number: JC1220; MUID:92392379; PMID:1325794
A:Accession: JC1221
A:Molecule type: mRNA
A:Residues: 1-179 <UEK>
A:Cross-references: GB:S43865; NID:g255080; PIDN:AAB23172.1; PID:g255081
A:Experimental source: Testis
C:Comment: With calcineurin catalytic chain plays an important role in neural and nonne
C:Genetics:
A:Gene: PP2B-beta-2
A:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
F:2-179/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
Query Match 14.4%; Score 130.5; DB 2; Length 179;
Best Local Similarity 24.5%; Pred. No. 9.8e-05;
Matches 37; Conservative 26; Mismatches 75; Indels 13; Gaps 3;
QY 35 CELLPQEQ-----RVVESLRQVPEQILSLPELKANPFKERICRVFSTSPAKDSL 86
Db 12 CNHFDQEEIRRLGKSFRLDKSGSLSTEERMLPELQONPLVGRVIDIFDTD-NGEV 70
QY 87 SPEDFDLLSVFSDTATPKIKSHYAFRIFFXXXXXXXSRVLNCLTGEGETRLSA 146
Db 71 DFHEFTVGTQSVRGDEQKLFAPRIYDMNDGFIISNGELFQVLKMMVG----NNLK 126
QY 147 SEMQLIDNILESDIDRDGTINLSEFQHV 177
Db 127 WQLQQLVDSKILVLDKDGGRISFEFSDV 157

Search completed: January 17, 2003, 12:46:52
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:38 ; Search time 12 seconds
(without alignments)
660.165 Million cell updates/sec

Title: US-09-878-454a-2x
Perfect score: 904
Sequence: 1 MGSGSRLSKELLAEYODLT.....EFOHVHSRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	879	97.2	191 1	KIP1_HUMAN
2	831	91.9	191 1	KIP1_MOUSE
3	830	91.8	191 1	KIP1_RAT
4	302	33.4	187 1	KIP2_MOUSE
5	299	33.1	187 1	KIP2_HUMAN
6	176.5	19.0	177 1	CALB_NAEGR
7	171.5	19.0	174 1	CALB_SCHPO
8	160.5	17.8	174 1	CALB_NECRO
9	159.5	17.6	174 1	CALB_YEAST
10	146.5	16.2	169 1	CALB_HUMAN
11	146.5	16.2	169 1	CALB_MOUSE
12	136.5	15.1	170 1	CALC_MOUSE
13	135	14.9	194 1	CA22_MOUSE
14	132.5	14.7	170 1	CALB_DROME
15	131	14.5	194 1	CA22_HUMAN
16	130.5	14.4	178 1	CALC_MOUSE
17	130	14.4	214 1	TESC_HUMAN
18	128.5	14.2	175 1	CALC_RAT
19	128	14.2	214 1	TESC_MOUSE
20	123.5	13.7	189 1	NCS2_CAEEL
21	121.5	13.4	186 1	FREQ_DROME
22	112	12.4	190 1	VIS2_RAT
23	112	12.4	192 1	VIS3_MOUSE
24	111	12.3	192 1	VIS3_CHICK
25	111	12.3	192 1	VIS3_HUMAN
26	109	12.1	189 1	NCS1_HUMAN
27	109	12.1	189 1	NCS1_XENLA
28	108	11.9	190 1	APIC_APICA
29	107.5	11.9	195 1	H520_HUMAN
30	103	11.4	190 1	VIS1_HUMAN
31	103	11.4	192 1	NCAH_MOUSE
32	101	11.2	189 1	NCAH_DROME
33	101	11.2	190 1	NCS1_CAEEL

ALIGNMENTS

RESULT 1
ID KIP1_HUMAN STANDARD; PRT: 191 AA.
AC 099628; 000735; 000693; 099971; 096354;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK interacting protein 2-28) (SIP2-28).
DE CIB1 OR PRKDCIP OR KIP OR CIB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_Taxid-9606;
OX NCB1_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein, KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE-Fetal liver;
RC MEDLINE=97184102; PubMed=9030514;
RA Naik U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=20284952; PubMed=10826701;
RA Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting protein (KIP).";
RL DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191.
RA MEDLINE=20285134; PubMed=10822252;
RA Hwang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and the alpha1b-integrin cytoplasmic domain suggest a mechanism for calcium-regulated recognition: homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 91.9%; Score 831; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 5,6e-72;
 Matches 168; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGGSGRLSKELLAEYODLFTLKQETLLAHRFCCLLPQEQTVSSRAQVPEQILS 60
 DB 1 MGGSGRLSKELLAEYODLFTLKQETLLAHRFCCLLPQEQTVSSRAQVPEQILS 60
 QY 61 LPELKNPKERKICWFSTSPAKDSISFEDFLDLSVSFSDTATPDIKSHYARIFEDDD 120
 DB 61 LPELKNPKERKICWFSTSPAKDSISFEDFLDLSVSFSDTATPDIKSHYARIFEDDD 120
 QY 121 XXXXXXXXRLVNCITGEGEDTRLASSEMKQILDNLEESDIDROGTINLSEFOHYSRS 180
 DB 121 GTLDREDSQLVNCITGEGEDTRLASSEMKQILDNLEESDIDROGTINLSEFOHYSRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 RA Kauselmann G, Weller M, Wulff P, Jessberger S, Konietzko U,
 RA Scafield J, Staudl U, Bepeler-Hahn J, Strebhardt K, Kuhl D;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539 (1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AF136585; AAF08368.1;
 DR HSSP; Q99828; IDGV
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MW; 3B00B0228879FC7 CRC64;

Query Match 91.8%; Score 830; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 7e-72;
 Matches 168; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGGSGRLSKELLAEYODLFTLKQETLLAHRFCCLLPQEQTVSSRAQVPEQILS 60
 DB 1 MGGSGRLSKELLAEYODLFTLKQETLLAHRFCCLLPQEQTVSSRAQVPEQILS 60
 QY 61 LPELKNPKERKICWFSTSPAKDSISFEDFLDLSVSFSDTATPDIKSHYARIFEDDD 120
 DB 61 LPELKNPKERKICWFSTSPAKDSISFEDFLDLSVSFSDTATPDIKSHYARIFEDDD 120
 QY 121 XXXXXXXXRLVNCITGEGEDTRLASSEMKQILDNLEESDIDROGTINLSEFOHYSRS 180
 DB 121 GTLDREDSQLVNCITGEGEDTRLASSEMKQILDNLEESDIDROGTINLSEFOHYSRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 DE
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain, and Testis;
 RX MEDLINE=99132027; PubMed=9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 RA Salto T.;
 RT "Structure, expression profile and chromosomal location of an isoolog
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Biochim. Biophys. Acta 144:143-147 (1999).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AB016080; BAA36545.1;
 DR HSSP; Q99828; IDGV
 DR MGD; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBD086F5C CRC64;

Query Match 33.4%; Score 302; DB 1; Length 187;
 Best Local Similarity 34.3%; Pred. No. 9.2e-22;
 Matches 69; Conservative 43; Mismatches 61; Indels 28; Gaps 6;

QY 1 MGGSGRLSKELLAQVQDFTFTKQELLAAHRRFCE---LLPQORTVSSSLRAQVPFE 56
 DB 1 MGNKQTIETFEQDLDNYQDCTFFNKDKILKHLHRRFYELAPNLVPMYR---KSPIVHVPM 57
 QY 57 QILSLPELKANPFRKICRVFSTSPAKDSLSPEDFLDLSVFSDDTATPDIKSHYAFRIFX 116
 DB 58 LIQMPRELNPFRKIVAAFS-EDGEGLNTENDFVDFSVLCESAPRELKANYAFKIYD 116
 QY 117 XXXXXXXXXXSLRVNCLTGGED---TRLSASEMKQ-----LIDNILEESDIDRDGTI 168
 DB 117 FNTD-----NFTCKEDLETLARLTKSELEDEEVVLVCDKVIEEADLDGDKL 164
 QY 169 NLSEFOHVISRSPDFASSFKI 189
 DB 165 GFADEFMIAKAPDFLSTFHI 185

RESULT 5
 KIP2_HUMAN STANDARD; PRT; 187 AA.
 AC 075838;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=99132027; PubMed=9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 of DNA-PKcs interacting protein (KIP) gene.";
 RL Biochim. Biophys. Acta 1444:143-147(1999).
 CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 or send an email to license@isb-sib.ch).
 DR EMBL; AB012955; BAA33584.1; -
 DR HSP; Q99828; IDGV.
 DR MIM; 605564; -
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21643 MW; D51F6C25AD381BEF CRC64;

Query Match 33.1%; Score 299; DB 1; Length 187;
 Best Local Similarity 34.3%; Pred. No. 1.8e-21;
 Matches 69; Conservative 42; Mismatches 62; Indels 28; Gaps 6;

QY 1 MGGSGRLSKELLAQVQDFTFTKQELLAAHRRFCE---LLPQORTVSSSLRAQVPFE 56
 DB 1 MGNKQTIETFEQDLDNYQDCTFFNKDKILKHLHRRFYELAPNLVPMYR---KSPIVHVPM 57
 QY 57 QILSLPELKANPFRKICRVFSTSPAKDSLSPEDFLDLSVFSDDTATPDIKSHYAFRIFX 116
 DB 58 LIQMPRELNPFRKIVAAFS-EDGEGLNTENDFVDFSVLCESAPRELKANYAFKIYD 116
 QY 117 XXXXXXXXXXSLRVNCLTGGED---TRLSASEMKQ-----LIDNILEESDIDRDGTI 168
 DB 117 FNTD-----NFTCKEDLETLARLTKSELEDEEVVLVCDKVIEEADLDGDKL 164
 QY 169 NLSEFOHVISRSPDFASSFKI 189
 DB 165 GFADEFMIAKAPDFLSTFHI 185

Db 1 MGNKQTIETFEQDLDNYQDCTFFNKDKILKHLHRRFYELAPNLVPMYR---KSPIVHVPM 57
 QY 57 QILSLPELKANPFRKICRVFSTSPAKDSLSPEDFLDLSVFSDDTATPDIKSHYAFRIFX 116
 Db 58 LIQMPRELNPFRKIVAAFS-EDGEGLNTENDFVDFSVLCESAPRELKANYAFKIYD 116
 QY 117 XXXXXXXXXXSLRVNCLTGGED---TRLSASEMKQ-----LIDNILEESDIDRDGTI 168
 Db 117 FNTD-----NFTCKEDLETLARLTKSELEDEEVVLVCDKVIEEADLDGDKL 164
 QY 169 NLSEFOHVISRSPDFASSFKI 189
 Db 165 GFADEFMIAKAPDFLSTFHI 185

RESULT 6
 CALB_NAEGR STANDARD; PRT; 177 AA.
 AC P42322;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit (protein phosphatase 2B regulatory subunit)
 DE (Calcineurin regulatory subunit).
 GN CNB1.
 OS Naegleria gruberi.
 OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
 OX NCBI_TaxID=5762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEG.
 RX MEDLINE=99137399; PubMed=7867946;
 RA Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;
 RT "A calcineurin-B-encoding gene expressed during differentiation of
 the amoeboid flagellate Naegleria gruberi contains two introns.";
 RL Gene 154:39-45(1995).
 CC -!- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN. A CALCIUM-DEPENDENT,
 CALMODULIN-REGULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 SENSITIVITY (BY SIMILARITY).
 CC SUBUNIT (B) (BY SIMILARITY).
 CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 SITES (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 or send an email to license@isb-sib.ch).
 DR EMBL; U04380; AAA81896.1; -
 DR HSP; P06705; LAUT.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 4.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).
 FT CA_BIND 70 81 EF-HAND 2 (BY SIMILARITY).
 FT CA_BIND 107 118 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 177 AA; 20057 MW; 01D4A48E6947E97C CRC64;

Query Match 19.5%; Score 176.5; DB 1; Length 177;
 Best Local Similarity 26.4%; Pred. No. 7.1e-10;
 Matches 47; Conservative 37; Mismatches 81; Indels 13; Gaps 3;

QY 1 MGGSGRLSKELLAQVQDFTFTKQELLAAHRRFCE---LLPQORTVSSSLRAQVPFE 56
 DB 1 MGNKQTIETFEQDLDNYQDCTFFNKDKILKHLHRRFYELAPNLVPMYR---KSPIVHVPM 57
 QY 57 QILSLPELKANPFRKICRVFSTSPAKDSLSPEDFLDLSVFSDDTATPDIKSHYAFRIFX 116
 DB 58 LIQMPRELNPFRKIVAAFS-EDGEGLNTENDFVDFSVLCESAPRELKANYAFKIYD 116
 QY 117 XXXXXXXXXXSLRVNCLTGGED---TRLSASEMKQ-----LIDNILEESDIDRDGTI 168
 DB 117 FNTD-----NFTCKEDLETLARLTKSELEDEEVVLVCDKVIEEADLDGDKL 164
 QY 169 NLSEFOHVISRSPDFASSFKI 189
 DB 165 GFADEFMIAKAPDFLSTFHI 185

```

DB 1 MGTNTSLRPEVEEOKTNTFTQKEIKLYRFRKLDKDGKTSK-----DEFLM 52
OY 61 IPELKNPFRKICRVFSTSPAKDSLSPEDFLDLVSFSDTAPDPSKHYARIFKXXXX 120
DB 53 IPELAVNPLVKAVISIFDEN-GDGSVNFKEFIALSVFAAGDQKCKLEFAKRYVIDD 111
OY 121 XXXXXXXXSRVNCITGEGEDTRLSASEMKQIDNILEESDIDRGTINLSEFOHVS 178
DB 112 GYISNGELFTVYKMAVG-----NNLSVDVQLQIVDKTILEADBDGDKISFEERAKTLS 165

RESULT 7
CALB_SCHPO STANDARD: PRT: 174 AA.
AC 090093:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcineurin B subunit (protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB1 OR SPC830.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE-2184601; PubMed-118959360;
RA Wood V., Williams R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Butler S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Wajsbom I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandt R., Punnett B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).

-1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
SENSITIVITY (BY SIMILARITY).
-1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
SUBUNIT (B) (BY SIMILARITY).
-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES (BY SIMILARITY).
-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL: AL109850; CAB52879.1; -.
DR HSSP: P06705; IAU1.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF_HAND; 4.
DR Calcium-binding; Myristate.
KW CA_BIND 34 45 EF_HAND 1 (BY SIMILARITY).
FT CA_BIND 66 77 EF_HAND 2 (BY SIMILARITY).
FT CA_BIND 103 114 EF_HAND 3 (BY SIMILARITY).
FT CA_BIND 144 155 EF_HAND 4 (BY SIMILARITY).
SQ SEQUENCE 174 AA: 19675 MW: EEP38EF74959442E CRC64;

Query Match 19.0%; Score 171.5; DB 1; Length 174;
Best Local Similarity 24.4%; Pred. No. 2,1e-09;
Matches 44; Conservative 43; Mismatches 76; Indels 17; Gaps 4;

OY 1 MGSGSRSLKELIAYODITFLTKOELLAHRRFCELLPQEQRYVESSIRAOVPEQILS 60
DB 1 MGOSQOIFEDLISN-----SFSNEIERIRRRRTK-----IDANQGSIDRNEFLS 48
OY 61 IPELKNPFRKICRVFSTSPAKDSLSPEDFLDLVSFSDTAPDPSKHYARIFKXXXX 120
DB 49 IPSVANPLASRLFSVDEDDGGD-VDFQFTNSLSVSVHGKKEKLEFAKRYVIDD 107
OY 121 XXXXXXXXSRVNCITGEGEDTRLSASEMKQIDNILEESDIDRGTINLSEFOHVS 180
DB 108 GYISNGELFTVYKMAVG-----TNLRDQLQIVDKTILEADBDGDKISFEERAKTLS 163

RESULT 8
CALB_NEUCR STANDARD: PRT: 174 AA.
AC P87072; 013408.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB-1 OR CAN-B.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-74A.
RX MEDLINE-96007857; PubMed-9349701;
RA Prokisch H., Yarden O., Dieminger M., Tropeschung M., Barthelmeis I.B.;
RT "Impairment of calcineurin function in Neurospora crassa affects its
RT essential role in hyphal growth, morphology and maintenance of the
RT apical Ca2+ gradient.";
RL Mol. Gen. Genet. 256:104-114(1997).

-1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
SENSITIVITY.
-1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
SUBUNIT (B) (BY SIMILARITY).
-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES.
-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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DB 1 GAAPSKIVDGLLED---TNPDRDEIERLKRFRMKLDRDSSGSSIDKN-----EFMSI 48
 QY 62 PELKANPKERICRYESTSPANKDSIFDELDLLSVFSPTAPPDIKSHAFIEFXXXXX 121
 DB 49 PGVSNPLAGRIMEYFDADNSGD-VDFQEFITGLSIFSGRSGDKERLRFKFIYDIDKDG 107
 QY 122 XXXXXXXXRLVNCLEGEDETRLSASEKKOLIDNILEESDIDRDGTINLSEFOHY 177
 DB 108 FISNGELFIVKIMWG-----SNLDEQLOQIYDRIVENDSDGDRLSFEFKNAI 159
 RESULT 10
 CALB_HUMAN STANDARD: PRT: 169 AA.
 AC P06705; P15117; Q08044;
 DT 01-JAN-1988 (Rel. 06, Cited)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calciineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
 GN PPP3R1 OR CNB OR CNA2.
 OS Homo sapiens (Human).
 OS Bos taurus (Bovine), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606, 9913, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE=90126237; PubMed=2558868;
 RA Guerini D., Krinks M.H., Sikelä J.M., Hahn W.E., Klee C.B.;
 RT "Isolation and sequence of a cDNA clone for human calciineurin B, the
 RT Ca²⁺-binding subunit of the Ca²⁺/calmodulin-stimulated protein
 RT phosphatase.";
 RL DNA 8:675-682(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RA Nargang C.E., Botoroff D.A., Adachi K.;
 RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-168.
 RC SPECIES-Bovine; TISSUE-Brain;
 RX MEDLINE=84132092; PubMed=6321104;
 RA Aitken A., Klee C.B., Cohen P.;
 RT "The structure of the B subunit of calciineurin.";
 RL Eur. J. Biochem. 139:663-671(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
 RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES-Rat; TISSUE-Brain, and Testis;
 RX MEDLINE=94153993; PubMed=8110831;
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory
 RT subunit of Ca²⁺/calmodulin-dependent protein phosphatase (calciineurin
 RT B alpha 2).";
 RL Biochim. Biophys. Acta 121:174-180(1994).
 RN [6]
 RP CALCIUM-BINDING DATA.
 RC SPECIES-Bovine;
 RX MEDLINE=80101597; PubMed=293720;
 RA Klee C.B., Crouch T.H., Krinks M.H.;
 RT "Calciineurin: a calcium- and calmodulin-binding protein of the
 RT nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RC SPECIES-Bovine;
 RX MEDLINE=95360994; PubMed=7543369;
 RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,
 RA Fitzgibbon M.J., Fleming M.A., Capon P.R., Hsiao K., Navia M.A.;
 RT "X-ray structure of calciineurin inhibited by the immunophilin-
 RT immunosuppressant FKBP12-FK506 complex.";
 RL Cell 82:507-522(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES-Human;
 RX MEDLINE=96097077; PubMed=8524402;
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempezyk A., Kalish V.J., Tucker K.D., Showalter R.E., Mooney E.W.,
 RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
 RA Baquer R., Villafraña J.E.;
 RT "Crystal structures of human calciineurin and the human FKBP12-FK506-
 RT calciineurin complex.";
 RL Nature 378:641-644(1995).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.
 CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC
 CC EMBL; M30773; AAB08721.1; -
 CC EMBL; X71666; CAA50659.1; -
 CC EMBL; L03554; AAA40854.1; -
 CC EMBL; D14568; BAA03422.1; -
 CC EMBL; D14425; BAA03318.1; -
 CC PIR; A33391; A33391.
 CC PIR; S34127; S34127.
 CC PIR; J70297; J70297.
 CC PIR; S42716; S42716.
 CC PIR; S42717; S42717.
 CC PDB; 1A0T; 03-DEC-97.
 CC PDB; 1TCO; 12-FEB-97.
 CC Genew; HGNC:9317; PPP3R1.
 CC MIM; 601302; -
 CC InterPro: IPR002048; EF-hand.
 CC Pfam: PF000036; efhand; 4.
 CC ProDom; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFh; 4.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC KMW Calcium-binding; Repeat; Alternative splicing; Myristate;
 CC 3D-structure.
 CC INIT_MER 0 0
 CC LIPID 1 1
 CC CA_BIND 30 41
 CC CA_BIND 62 73
 CC CA_BIND 99 110
 CC CA_BIND 140 151
 CC VARSPLIC 1 1
 CC
 CC CONFLICT 11 11
 CC CONFLICT 153 153
 CC SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
 CC
 CC Query Match 16.2%; Score 146.5; DB 1; Length 169;
 CC Best Local Similarity 27.0%; Pred. No. 4, 8e-07;

[illegible]

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
 CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
 CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONTERS CALCIUM
 CC SENSITIVITY (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL: U56245; AAC47350.1; -
 DR EMBL: AEO03840; AAF59195.1; ALT_SEQ.
 DR HSP: P06705; LTCO.
 DR FlyBase: Fgn0015614; Canb2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; Eph; 4.
 DR PROSITE: PS00018; EF_HAND; 4.
 DR Calcium-binding; Repeat.
 FT CA_BIND 31 42 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 63 74 EF_HAND 2 (POTENTIAL).
 FT CA_BIND 100 111 EF_HAND 3 (POTENTIAL).
 FT CA_BIND 141 152 EF_HAND 4 (POTENTIAL).
 FT CA_BIND 170 AA; 19267 MW; FDBIBD9B5A4BDEC CRC64;
 SQ SEQUENCE
 Query Match 15.1%; Score 136.5; DB 1; Length 170;
 Best Local Similarity 21.9%; Pred. No. 4,3e-06;
 Matches 39; Conservative 39; Mismatches 81; Indels 19; Gaps 4;
 Oy 3 GGSGLSKELLAEYODLTLTKOETLLARPCCELLPOBOFTVSSLRQVPEQLSLP 62
 Db 2 GNETSLPEMCSNFD-----ADEIRLRGKRF-----RKLDLNSGALSDERMSP 47
 Oy 63 EKANPFEKRICRVSTSPAKDSLFEEDLDLVSVDATADPIKSHVAFRIFFXXXXXX 122
 Db 48 ELQGNPLVQRYVIDFD-ADGNGEYVDFKEIGVSQFSYVGDLSKIRFAFRITMDNDGY 106
 Oy 123 XXXXXXSLVNLGEGEETRLSASEMQLINILEESIDIDRGITNLSFCHVYSRS 180
 Db 107 ISNGELFVLMKMGV-----NNLKDTQLOOIYDKTIGFADKDEGKISFEFCVAGNT 160
 RESULT 13
 CA22_MOUSE
 ID CA22_MOUSE STANDARD; PRT; 194 AA.
 AC Q62877;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (S14470).
 GN CHP.
 OS Mus musculus (Mouse), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid:10090, 10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC SPECIES-Rat; TISSUE-Liver;
 RA MEDLINE-96215311; PubMed-8626580;
 RX Barroso M.R., Bernd K.K., Dewilt N.D., Chang A., Mills K.,
 RA Szul E.S.,
 RT "A novel Ca2+-binding protein, p22, is required for constitutive
 RT membrane traffic."
 RL J. Biol. Chem. 271:10183-10187(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC SPECIES-Rat; TISSUE-Brain;
 RA MEDLINE-21374135; PubMed-11481038;
 RX Matsumoto M., Miyake Y., Nagata M., Inoue H., Shitkubo D.,
 RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.,
 RT "A serine/threonine kinase which causes apoptosis-like cell death
 RT interacts with a calcineurin B-like protein capable of binding Na+/H+
 RT exchanger."
 RL J. Biochem. 130:217-225(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC SPECIES-Mouse;
 RA Saito T., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.,
 RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RC SPECIES-Mouse; STRAIN-C57BL/6J; TISSUE-Liver;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kaval T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hornann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Mazarrelli J., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokura K., Wang K.H., Weitz C., Whitaker C., Williams L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
 CC -1- PFM: BOTH N-WRISTOLYATION AND CALCIUM-MEDIATED CONFORMATIONAL
 CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC -----
 DR EMBL: U39875; AB04146.1; -
 DR EMBL: AB070350; BAB63369.1; -
 DR EMBL: AB025217; BAA84688.1; -

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DR EMBL; AK005067; BAB23791.1;
DR HSSP; P06705; LAUT.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF-HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0
FT LIPID 1
FT DOMAIN 38 49 MYRISTATE (PROBABLE).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT CA_BIND 122 133 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 163 174 EF-HAND 3 (BY SIMILARITY).
FT MUTAGEN 133 133 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 194 AA; 22301 MW; 1E2DF35F627B8331 CRC64;

Query Match 14.9%; Score 135; DB 1; Length 194;
Best Local Similarity 24.2%; Pred. No. 6.9e-06;
Matches 47; Conservative 31; Mismatches 84; Indels 32; Gaps 6;

QY 5 GSR-----LSKELLAAYODLFLKQKELLAAHRRFCCLLPQEQRTVSSLRQVFFQILS 60
DB 1 GSRATLLRDELEFEIKKETGFSHQITRLYSRFTSLDKGNGTLR-----EDFQR 52
QY 61 LPEKANPFERICRVSTSPAKDSLSFDFDLVSVF-----SDTATPD----- 105
DB 53 IPELAINPLGDRINAF-FSEGEDQVNFGRFMTLAHFRIDNEKSKDVNGPEPLNSRS 111
QY 106 IKSHVAFRIEYXXXXXXXXXXXXXXXXXSRVNCITGEGEDTRLSASEMKQLIDNILESDIDRD 165
DB 112 NKLHFAFLYDLDDKISRDELQVLRMMVG-----VNISDEQLGSIADRTIQEADQGD 167
QY 166 GTINLSEFQHVISR 179
DB 168 SAISFTFVKVLEK 181

RESULT 14
ID CALB_DROME STANDARD; PRT; 170 AA.
AC P48451; OSW4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 401, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
DE CANB OR CANB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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QY 86 LSFEDFLDLVSPTATPDIKSHVAFRIEXXXXXXXXRLVNCITGEGEDTRLS 145
 DB 70 VEFKEFIGVSOFSVGRDLKSLRFAFRIDYMDNDGYSINGELFYVLMKMGV----NNLK 125
 QY 146 ASEMKOLIDNILEESDIDBDGTINLSEFQHVISR 180
 DB 126 DTLOOIYDKTICFADKDEGKISFEFCVVGNT 160

RESULT 15
 CA22_HUMAN STANDARD: PRT: 194 AA.
 AC Q99653:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog)
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X, Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL: U61538; AAB37770.1;
 DR EMBL: BC001646; AAH01646.1;
 DR HSSP: P06705; LAUI.
 DR MIM: 606988;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 3.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
 DR Calcium-binding; Repeat; Myristate; Phosphorylation.
 DR INIT_MET 0
 FT LIPID 1
 FT 1 MYRISTATE (BY SIMILARITY).
 FT 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT DOMAIN

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDEBF03C86380 CRC64;
 Query Match
 Best Local Similarity 23.7%; Pred. No. 1.7e-05;
 Matches 46; Conservative 31; Mismatches 85; Indels 32; Gaps 6;
 14.5%; Score 131; DB 1; Length 194;
 QY 5 GSR----LSKELAEYQDITFLTKQEBLLAHRRFCCLLPQORTVSSSLRAQVPEQLIS 60
 DB 1 GSRASYLLRDEDELEKEIKETGFSHQITRLYSRFTSLDGENGTLSR-----EDPR 52
 QY 61 LPELKNPFKERICRYFSTSPAKDSLSEDFDLDSVF-----SPTATPD----- 105
 DB 53 IPELATNPGLGRITNAFPE-GEQVNFEGFMATLAHFPIEDNEKSKVNGPEPLNSRS 111
 QY 106 IKSHVAFRIEXXXXXXXXRLVNCITGEGEDTRLSASEMKOLIDNILEESDIDBD 165
 DB 112 NKLIHFAFRITDLDKDKISRDELLOVLRMGV----VNISDQLGSIAORTTQEDAQDSD 167
 QY 166 GTINLSEFQHVISR 179
 DB 168 SAISFTEFYKYLEK 181

Search completed: January 17, 2003, 12:45:50
 Job time: 13 secs

GenCore version 5.1.3.
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:58 ; Search time 31 Seconds
(without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MGSGSRLSKELLAEYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_proteint:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	40.6	311	5	Q93640
2	318	35.2	185	11	Q96095
3	310	34.3	187	4	Q96077
4	297.5	32.9	206	5	Q9W205
5	194	21.5	54	6	Q9GLJ2
6	188.5	20.9	180	5	Q9GP83
7	161	17.8	175	10	Q93VR2
8	161	17.8	175	10	Q9LS47
9	159	17.6	175	5	Q9U0X7
10	144.5	16.0	169	5	Q9NFN1
11	144.5	16.0	244	5	Q20804
12	140.5	15.5	170	5	Q9NKM7
13	140.5	15.5	195	5	Q23643
14	140	15.5	29	11	Q99J75
15	138.5	15.4	213	5	Q16343
16	138.5	15.3	170	5	Q95P81

17	137.5	15.2	115	11	Q99J75	Q99J75 mus musculu
18	137	15.2	274	10	Q9AMT4	Q9AMT4 oryza sativ
19	136	15.0	200	5	Q8SRF8	Q8SRF8 encephalit
20	134	14.8	214	11	Q8VCM1	Q8VCM1 mus musculu
21	133.5	14.8	213	10	Q9LTF8	Q9LTF8 arabidopsi
22	132.5	14.7	175	3	Q9HDE1	Q9HDE1 cryptococcu
23	132.5	14.7	177	3	Q9HDE1	Q9HDE1 cryptococcu
24	130.5	14.4	226	10	Q81446	Q81446 arabidopsi
25	130	14.4	170	4	Q8WYJ4	Q8WYJ4 homo sapien
26	130	14.4	173	4	Q96LZ3	Q96LZ3 homo sapien
27	127	14.0	216	4	Q9NMT9	Q9NMT9 homo sapien
28	126.5	14.0	161	10	Q9AY39	Q9AY39 homo sapien
29	126.5	14.0	187	5	Q9WYX8	Q9WYX8 oryza sativ
30	124.5	13.8	189	5	Q9VNF9	Q9VNF9 drosophila
31	122	13.5	190	3	Q96X50	Q96X50 magnaporthe
32	122	13.5	190	3	Q8TGC0	Q8TGC0 magnaporthe
33	121	13.4	191	4	Q9UM19	Q9UM19 homo sapien
34	121	13.4	192	10	Q81328	Q81328 arabidopsi
35	120	13.3	225	10	Q8W5C8	Q8W5C8 oryza sativ
36	119	13.2	196	5	Q9N2Y1	Q9N2Y1 caenorhabdi
37	118.5	13.1	226	10	Q81447	Q81447 arabidopsi
38	117	12.9	246	10	Q82641	Q82641 caenorhabdi
39	114.5	12.7	213	10	Q81445	Q81445 arabidopsi
40	112	12.4	190	5	Q9NAY9	Q9NAY9 neogleria f
41	111	12.3	214	10	Q9FVQ7	Q9FVQ7 arabidopsi
42	111	12.3	222	10	Q81223	Q81223 arabidopsi
43	111	12.3	224	10	Q9SGW7	Q9SGW7 arabidopsi
44	110.5	12.2	153	5	Q9U5J0	Q9U5J0 trichomonas
45	110.5	12.2	160	5	Q9U5I9	Q9U5I9 trichomonas

ALIGNMENTS

RESULT 1

ID Q93640 PRELIMINARY; PRT; 311 AA.

AC Q93640; 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE F30A10.1 protein.

GN F30A10.1

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peleoderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RA [1]

RP SEQUENCE FROM N.A.

RA Barlow K.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP MEDLINE=99069613; PubMed=9851916;

RA none;

RT Investigating biology of the nematode C. elegans: A platform for

RT Science 282:2012-2018(1998).

RL EMBL; 281072; CAB03019.1;

DR HSSP; Q98828; IDGV.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; EF-hand; 3.

DR Prodom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.

SO SEQUENCE. 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;

Query Match 40.6%; Score 367; DB 5; Length 311;

Best local Similarity 39.6%; Pred. No. 3.4e-30;

Matches 82; Conservative 39; Mismatches 60; Indels 26; Gaps 5;

OY 1 MGSGSRLSKELLAEYQDLTFTQELILAHRRCELLPOQRIVSS 48

DB 111 MGNNASSLSSELNLFSGGVFTREQLDEYDCFFETRKDIIRLYKRYALNPKR---VPTN 167

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Db   68 DRICRVFSD---NVFSFDVLGMASVFSQAQPSLKIEYAFRIYDFNENGFIDEEDLEE 120
Qy   131 LVNLCTGEGEDTRLRSASE--MKOLINDNILEESDIDRDTGTLINLSEFGHVRISRPDSFASSFK 188
      :| | : :| | : : :| | : : :| | : : :| | : : :| | : : :| | : : :| | :
Db   125 IYLRLL-KSDD---ASEDLLMDVMHVLSDESDDLNDNSMLSFSEFEHAKMSPDFWNSFR 179
Qy   189 I 189
      |
Db   180 I 180

RESULT 3
Q96Q77 PRELIMINARY; PRT; 187 AA.
AC Q96Q77
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE KIP3.
GN KIP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayashi A., Okaze H., Kozuma S., Saito T.;
RT "KIP3";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB050868; BAB71789.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF-HAND; UNKNOWN_2.
SQ SEQUENCE 187 AA; 21801 MW; FB32CCB46DF5ADCF CRC64;

Query Match 34.3%; Score 310; DB 4; Length 187;
Best Local Similarity 37.3%; Pred. No. 1.7e-24;
Matches 72; Conservative

Qy 1 MGGSGSRSLSKELAEYQDLFTLTQKEILLAHRRCELLPQ-----EQFTVFSSLRQAYPFE 56
    || : : :| | | | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Db 1 MGNTQTVTFHQLEAYQDCUFTFKETKRMLFYRYQDLAPQLVDYTTCPD---VKVPYE 57
    || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Qy 57 OILSPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVSFSTATPDIKSHYAFRIFX 116
    || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Db 58 LIGSNPELKDNPPFQRQTAAQVES-EDGDGHMTLDNFLDMFWSWKAPRDULKAYAFKIYD 116
    || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Qy 117 XXXXXXXXXXXXXRLVNCLTGEGETTRLSAEMKQLDNIILESDIDRDTGTINLSEFOHV 176
    || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Db 117 FNNDYICAWDLEQTVTKLTRGG---LSAEVSVLCVKELVDAGDHGDGRSLSEDQNFM 177
    || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :
Qy 177 ISRSPDFASSFKI 189
    | :| | | :| |
Db 173 ILRAPDFLSTFH 185

RESULT 4
Q9W2Q5 PRELIMINARY; PRT; 206 AA.
AC Q9W2Q5
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG9236 protein.
GN CG9236.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
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[illegible]


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Q9U0X7
ID Q9U0X7 PRELIMINARY; PRT; 175 AA.
AC Q9U0X7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Calcineurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_Taxid=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Tosato V., Bruschi C.V., Iyans A.C., Murphy L., Quail M.,
RA Rajendram M.A., Barrell B.G.,
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Smith D.F.;
RA "A physical map of the Leishmania major Friedlin genome.";
RL EMBL: AL133435; CAB62809.1;
DR HSSP: P06705; IAU.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; Eph; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN.2.
SQ SEQUENCE: 175 AA; 19660 MW; 9448F127FADFA0EB CRC64;

Query Match
Best Local Similarity 22.5%; Score 159; DB 5; Length 175;
Matches 41; Conservative 41; Mismatches 86; Indels 14; Gaps 4;

QY 8 LSKELLAEVQDLFTLTKOELLAHRRFCELLPOEORTVESSLRAOVPEQILSLPELKAN 67
DB 6 LAAEQLNIRESTALTDAGVQRLYKSFSL-----NKDKSGKITRAEFNSIPALASN 57
QY 68 PKERICRFVSTSPAKDSLSEFEDLLSVFSTATPDIKSHYAFRIYXXXXXXX 127
DB 58 PLVDRLAVAMDID-GDSTVDFGFRALAVLSATSKEDELRFTFKYDVDDGGRISNKKD 116
QY 128 XRLVNLCTGEGEDTRLASSEMQLDNLLESDIDRDGTINLSEFOHVISRPPDRASSF 187
DB 117 LFOMLSIMVG-----VNLSONQLOQIVDKTFIEADVDRDGTTFEERQ-ALAVNSDFGDL 171
QY 188 KI 189
DB 172 NL 173

RESULT 10
Q9NFN1 PRELIMINARY; PRT; 169 AA.
AC Q9NFN1;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Calcineurin B.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoididae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20520966; PubMed=11071287;
RX Mecozzi B., Rossi A., Lazaretti P., Kady M., Kaiser S., Valle C.,

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RA C1011 D., Klinkert M.O.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT Immunolocalization to the excretory system.";
RL MCL. Biochem. Parasitol. 110:333-343(2000).
DR EMBL: AJ276885; CAB93677.1;
DR HSSP: P06705; ITCO.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; Eph; 4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN.4.
SQ SEQUENCE: 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match
Best Local Similarity 26.0%; Score 144.5; DB 5; Length 169;
Matches 32; Conservative 29; Mismatches 57; Indels 5; Gaps 2;

QY 56 EQLSLPELKNPKERICVSTSPAKDSLSEFEDLLSVFSTATPDIKSHYAFRI 115
DB 40 KEFWSLPELQNPVLAHVIEIFPTD-GNGEVDFKEFINGSQSANGKEAKLKFAFKRI 98
QY 116 XXXXXXXXXXXXSRVNLCTGEGEDTRLASSEMQLDNLLESDIDRDGTINLSEFOH 175
DB 99 DMKDGITSNGLFQYVLMKRVG---NNLMDTQLOQIVDKTFIEADVDRDGTTFEERQ 154
QY 176 VIS 178
DB 155 VVS 157

RESULT 11
Q20804 PRELIMINARY; PRT; 244 AA.
AC Q20804;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE F55C10.1 protein.
GN F55C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none.
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RT Science 282:2012-2018(1998).
DR EMBL: Z74036; CAA8489.2;
DR HSSP: P06705; IAU.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; Eph; 4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN.4.
SQ SEQUENCE: 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;

Query Match
Best Local Similarity 25.0%; Score 144.5; DB 5; Length 244;
Matches 45; Conservative 35; Mismatches 77; Indels 23; Gaps 6;

QY 3 GGSRLSKELLAEVQ-DLFTLTKOELLAHRRFCELLPOEORTVESSLRAOVPEQILS 60

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Db 75 GADASLPNMCNSFDVAVELRLT-----RRFKKL-----DVDSG--GSLSVVEEFMS 118
QY 61 LPKLANPFKRICRVFSTPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXX 120
Db 119 LPELQNPVLRVIDFD-EDNGEVDFREFIQISQFSVKGDKNKLKAFRIYDMRD 177
QY 121 XXXXXXSLRVNCLTGGEDTRLSASEMKQLIDNILEESDIDRGTINLSEFQHVIRS 180
Db 178 GFISNGELFQVLKMWG-----NNLKDSQLQIVDKTILFHDKDGDKGISFOEFCDVVEHT 233

RESULT 12
Q99KW7 Q99KW7 PRELIMINARY; PRT; 170 AA.
AC Q99KW7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcineurin B.
OS Pectinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Mizuhopecten.
OX NCBI_TaxID=6573;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;
RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from
RT Scallop Testis: Demonstration of Stage-Specific Expression during
RT Maturation of the Testis.";
RL J. Biochem. 0:0-0(2000).
DR EMBL; AB041524; BAA94543.1; -.
DR HSSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 170 AA; 19238 MW; 945032698470F44 CRC64;

Query Match 15.5%; Score 140.5; DB 5; Length 170;
Best Local Similarity 22.3%; Pred. No. 8.2e-07;
Matches 39; Conservative 39; Mismatches 78; Indels 19; Gaps 4;

QY 3 GSGSLSKELLAAYQDLTFLTKOEILLAHRRFCELLPQEQRTVSSSLRAQVPEQILSLP 62
Db 2 GNENSLPMELCSNFD-----PDEIKRLGRF-----RKLDLNSGSLSVDFEFTLP 47
QY 63 ELKANPFKERICRVFSTPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXX 122
Db 48 ELQNPVLRVIDFDFTD-NGGEVDFKEFTGVQSVKGDLSLKLRFKFIYDMDKGY 106
QY 123 XXXXXXSLRVNCLTGGEDTRLSASEMKQLIDNILEESDIDRGTINLSEFQHVIRS 177
Db 107 ISNGELFQVLKMWG-----NNLKDTQLQIVDKTIIHADADGDKGISFEFCVAV 157

RESULT 13
Q23643 Q23643 PRELIMINARY; PRT; 195 AA.
AC Q23643;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE ZK856.8 protein.
GN ZK856.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
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RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RN Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z70783; CAA94856.1; -.
DR HSSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 195 AA; 22670 MW; 9F4FDD6D8BD7BA88 CRC64;

Query Match 15.5%; Score 140.5; DB 5; Length 195;
Best Local Similarity 22.3%; Pred. No. 9.8e-07;
Matches 44; Conservative 40; Mismatches 82; Indels 31; Gaps 6;

QY 1 MGGSGS-RLSKELLAAYQDLTFLTKOEILLAHRRFCELLPQEQRTVSSSLRAQVPEQIL 59
Db 1 MGNSSSLMLRDEEIEIMSETFNRNQIVRLYSRFLSLDKKGQGLSR-----DDFL 52
QY 60 SLPELANPFKERICRVFSTSPA-----KDSLSFEDFLDLSVFSDTATPDIKSH---- 109
Db 53 NYPELANPGLRIVDAFFETLASSNGDNEQQLNFRQVIRILAHFQPISR--VKKNALNS 110
QY 110 -----YAFRIFFXXXXXXXSRVNLNLTGEGEDTRLSASEMKQLIDNILEESDID 163
Db 111 RDKLLFAKMYDLNKNYITREEFKVLNSMVG-----ANITSDQLDKIADRIEADAD 166
QY 164 RDGTINLSEFQHVIRS 180
Db 167 RDKGISFEFCRAVEKT 183

RESULT 14
Q99JY5 Q99JY5 PRELIMINARY; PRT; 29 AA.
AC Q99JY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein kinase, DNA activated, catalytic polypeptide
DE interacting protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005570; AAH05570.1; -.
DR HSSP; Q99828; IDGV.
KW Kinase.
SQ SEQUENCE 29 AA; 3242 MW; E19D6177AF420612 CRC64;

Query Match 15.5%; Score 140; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKOEILL 29
Db 1 MGGSGSRLSKELLAAYQDLTFLTKOEILL 29

RESULT 15
O16343
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ID 016343 PRELIMINARY; PRT; 213 AA.
AC 016343;
DT 01-JAN-1998 (TEMBREL. 05, Created)
DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
DT 01-MAR-2002 (TEMBREL. 20, Last annotation update)
DE F59D6.7 protein.
GN F59D6.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; Pubmed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Koopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Wellstock L., Wilkinon-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Bradshaw H., Graves T.;
RT "The sequence of C. elegans cosmid F59D6."
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF016435; AAB5882.1; -
DR HSSP, P06705; IAU1.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; efhand; 4.
DR ProDom: PD000012; EF-hand; 2.
DR SMART, SM00054; EFh; 2.
DR PROSITE, PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 213 AA; 24432 MW; AB19689122E91391 CRC64;

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Query Match          15.4%; Score 139.5; DR 5; Length 213;
Best Local Similarity 22.1%; Pred. No. 1.4e-06;
Matches 47; Conservative 40; Mismatches 81; Indels 45; Gaps 7;

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QY 1 MGS6SGSRL-----SKELLAEQ-----DLFTFKOEILLARRFCCLPQE 41
DB 1 MGSNSNSIISDAEMREIMDETQCKVCVIAKOPTPKNTISVKNHQLILYTRFASL----- 56
QY 42 QRTVESSLRAQVPFEEOILSLPELKANPFKEKICRVFSTSPAKD-----SLSFEDFLDL 95
DB 57 ----DKNGGYLSRDLFLVNPPLGRIIDAFETLGDSDGDSKSGQLTFRQFVRIL 112
QY 96 SYF-----SDTATPDIKS--HYAFRIFFXXXXXXXSRVLCNLTGEGEDTRLAS 147
DB 113 AHFOPIISKYKDNLNLSRKDKLRFAPFMVLDLNKNNTYTRREEFKVILNSWG----ANITSD 168
QY 148 EMKQILDLNLESDDIDRGTINLSEFOHVISRS 180
DB 169 QLDKIADKTLEADQDQDQKISFEDFCRAMKRT 201

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Search completed: January 17, 2003, 12:46:28
Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:49:00 ; Search time 35 Seconds

(without alignments)
727.168 Million cell updates/sec

Title: US-09-878-454a-2x

Perfect score: 904
Sequence: 1 MGSGSRSLKSLAEYODLT.....EFQVHNSRPFASFATKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	900	99.6	191	AAW51215	Amino acid sequence
2	892	98.7	191	AAW64199	Human interferon r
3	875	96.8	191	AAW62287	Human protein phos
4	354	39.2	172	AAU87324	Novel central nerv
5	354	39.2	184	AAW43562	Human polypeptide
6	352	38.9	185	AAW64418	Amino acid sequence
7	336	37.2	187	AAE09736	Human kinase inter
8	328	36.3	173	ABW96054	Human testicular a
9	328	36.3	173	AAU87612	Novel central nerv
10	328	36.3	173	AAW95362	Human reproductive

11	328	36.3	173	22	AAW43637	Human polypeptide
12	328	36.3	173	22	AAU19932	Novel human calcit
13	320.5	35.5	206	22	ABW64325	Drosophila melanog
14	225.5	24.9	169	23	ABP41194	Human ovarian anti
15	217	24.0	120	20	AAW11976	Human 5' EST secre
16	189.5	21.0	175	20	AAW00881	Calcineurin regula
17	189	20.9	175	21	AAW21178	zeae may protein f
18	189	20.9	210	21	AAW21177	zeae may protein f
19	186	20.6	175	23	AAW51586	Herbicidally activ
20	186	20.6	175	23	ABW92357	Arabidopsis thalia
21	184	20.4	175	21	AAW07824	Arabidopsis thalia
22	177	19.6	169	21	AAW51587	Arabidopsis thalia
23	175	18.4	169	21	AAW07825	Arabidopsis thalia
24	175	18.4	169	21	AAW21179	zeae may protein f
25	171.5	19.0	170	19	AAW64200	Human calcineurin
26	171.5	19.0	170	21	AAW09978	Human HCNB protein
27	158.5	17.5	162	22	ABW5554	Drosophila melanog
28	157.5	17.4	170	22	ABW60493	Arabidopsis thalia
29	156.5	17.3	226	21	AAW47032	Calcineurin B subu
30	155.5	17.2	226	21	AAW47033	Calcineurin B subu
31	155	17.1	170	22	AAW09977	Human CNBII protei
32	155	17.1	170	22	AAW01411	Human polypeptide
33	155	17.1	173	22	AAW64410	Novel human calcit
34	155	17.1	187	22	AAW87327	Drosophila melanog
35	155	17.1	189	22	ABW95936	Human testicular a
36	155	17.1	189	22	AAW87615	Human reproductive
37	155	17.1	189	22	AAW95239	Human polypeptide
38	155	17.1	189	22	AAW43564	Novel human calcit
39	155	17.1	189	22	AAW19951	Drosophila melanog
40	155	17.1	189	22	ABW61857	Drosophila melanog
41	151.5	16.8	187	22	ABW67063	Drosophila melanog
42	151.5	16.8	187	22	ABW67063	Drosophila melanog
43	149.5	16.5	192	23	ABW58936	Herbicidally activ
44	146	16.2	189	23	ABW92797	Arabidopsis thalia
45	144.5	16.0	226	21	AAW31315	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAW51215
ID AAW51215 standard; Protein; 191 AA.
AC AAW51215;
XX

DT. 21-AUG-1998 (first entry)

XX Amino acid sequence of the calcium-integrin binding protein.

DE Human calcium-integrin binding protein; CIB; integrin alpha IIB;
XX cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;

KW Inhibition; blood coagulation; vascular disorder.
KW
XX

XX Homo sapiens.
XX

OS Key Location/Qualifiers
FH Region 116..128
FT /note= "EF-hand motif"

FT Region 160..173
FT /note= "EF-hand motif"

XX W09814471-A1.

XX 09-APR-1998.

XX 24-SEP-1997; 97WO-US16828.

XX 02-OCT-1996; 96US-0720625.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Naik UP, Parise LV;
PI

XX WPI: 1998-240018/21.
 DR N-PSDB; AAV07211.
 XX New isolated calcium-integrin binding protein - is expressed in
 PT platelets and activates the fibrinogen receptor, used to develop
 PT products for treating e.g. vascular disorders
 XX Claim 1; Page 30; 44pp; English.
 PS This is the amino acid sequence of the human calcium-integrin binding
 CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
 CC domain. The CIB protein is expressed in platelets and interacts with
 CC the alpha IIB subunit of integrin alpha IIB-beta 3, to activate the
 CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
 CC activation of the fibrinogen receptor where it is desired to reduce
 CC blood coagulation for therapeutic, diagnostic or pharmaceutical
 CC reasons. The products can be used for treating vascular disorders,
 CC and for isolating or purifying integrins or fibrinogen. They can also
 CC be used for detection and diagnosis.
 XX Sequence 191 AA;
 SQ
 Query Match 99.6%; Score 900; DB 19; Length 191;
 Best Local Similarity 92.7%; Pred. No. 1.6e-81;
 Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGGSGRLSKELAEYQDLFTLTKQEIILAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
 DB 1 MGGSGRLSKELAEYQDLFTLTKQEIILAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFKEICRVSTSPAKDSLFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 DB 61 LPELKANPFKEICRVSTSPAKDSLFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFOHVIRS 180
 DB 121 GTLNREDLSRLVNLCTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFOHVIRS 180
 QY 181 PDFASSEFKIVL 191
 DB 181 PDFASSEFKIVL 191
 RESULT 2
 AAW64199
 ID AAW64199 standard; Protein; 191 AA.
 XX AAW64199;
 XX
 AC
 XX
 DT 09-NOV-1998 (first entry)
 XX Human interferon receptor 1 binding protein IR1B1.
 DE Interferon receptor 1 binding protein; IR1B1; human; tumour;
 XX cancer; gene therapy; tissue graft; graft survival.
 XX Homo sapiens.
 OS
 XX
 PN W09831796-A1.
 XX
 XX
 PD 23-JUL-1998.
 XX
 XX 15-JAN-1998; 98WO-US000671.
 PF
 XX
 PR 15-JAN-1997; 97US-0035636.
 XX
 XX (MCIN/) MCINNIS P A.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Abramovitch C, Chebath JE, Revel M;
 XX WPI: 1998-414096/35.
 DR

DR N-PSDB; AAV44272.
 XX New isolated interferon receptor binding proteins - used to develop
 PT products for modulating sensitivity to interferon, e.g. in the
 PT treatment of tumours or for prolonging graft survival
 XX Claim 1; Page 34; 64pp; English.
 PS This is a novel human protein, designated interferon receptor
 CC binding protein 1 (IR1B1), which interacts with the intracytoplasmic
 CC (IC) domain of the IFNAR1 chain of the interferon type 1 (IFN-alpha,
 CC beta or omega) receptor. IR1B1 is a new member of the calcineurin
 CC and calyculin family of calcium-regulated proteins (see also
 CC AAW64200). It is induced very rapidly and transiently following IFN
 CC treatment of human cells. It was identified in a two-hybrid
 CC screening for proteins interacting with the IFNAR1-IC domain;
 CC another protein, IR1B4 (see AAW64202), was similarly identified. A
 CC cDNA clone (see AAV44272) encoding IR1B1, host cells and expression
 CC vectors are claimed. DNA encoding IR1B1 and IR1B4 can be used in
 CC cancer therapy where the increased cellular response to IFN would
 CC result in a decrease in malignant cell growth and an enhanced
 CC response to exogenous IFN therapy. Antisense IR1B1 or IR1B4
 CC nucleic acids can be used for prolonging tissue or organ graft
 CC survival in patients as the rejection of these grafts in the host
 CC is mediated by the histocompatibility antigens (MHC class I) whose
 CC synthesis depends on the IFN stimulus. The products can also be
 CC used in detection and diagnosis.
 XX Sequence 191 AA;
 SQ
 Query Match 98.7%; Score 892; DB 19; Length 191;
 Best Local Similarity 92.1%; Pred. No. 1e-80;
 Matches 176; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGGSGRLSKELAEYQDLFTLTKQEIILAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
 DB 1 MGGSGRLSKELAEYQDLFTLTKQEIILAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFKEICRVSTSPAKDSLFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 DB 61 LPELKANPFKEICRVSTSPAKDSLFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXX 120
 QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFOHVIRS 180
 DB 121 GTLNREDLSRLVNLCTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFOHVIRS 180
 QY 181 PDFASSEFKIVL 191
 DB 181 PDFASSEFKIVL 191
 RESULT 3
 AAW62287
 ID AAW62287 standard; Protein; 191 AA.
 XX AAW62287;
 XX
 AC
 XX
 DT 24-SEP-1998 (first entry)
 XX Human protein phosphatase regulatory subunit.
 DE Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
 XX immunosuppression; neurodegeneration; inflammation; cancer.
 KW Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 44 /label= unknown
 FT /note= "encoded by ASG"
 FT Misc-difference 45 /label= unknown
 FT /note= "encoded by TGN"
 FT

XX PN WO9626056-A1.
 XX PD 18-JUN-1998.
 XX PF 25-NOV-1997; 97WO-US21603.
 XX PR 12-DEC-1996; 96US-0764563.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Goli SK, Hillman JL;
 XX DR WPI, 1998-348518/30.
 XX DR N-PSDB; V398009.
 XX PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
 XX PT prevention and treatment of immuno-suppression, neuro-degeneration,
 XX PT inflammation and cancer
 XX PS
 XX Claim 1; Fig 1; 65pp: English.
 CC The present sequence is a pure human protein phosphatase regulatory
 CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
 CC HCNB, are used to produce recombinant HCNB which is used to treat or
 CC prevent immunosuppression or neurological diseases (especially parasitic,
 CC bacterial or viral infections, including AIDS; the effects of radio- or
 CC chemo-therapy and Alzheimer's disease). Antagonists which bind
 CC specifically to HCNB and modulate its activity are used to treat
 CC inflammation, cancer, or immunological disorders and allograft rejection
 CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
 CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
 CC arthritis). Complements of the DNA encoding HCNB are useful as probes
 CC and primers for detecting the DNA encoding HCNB by hybridisation or
 CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
 CC particularly for diagnosis of the specified disorders, including early
 CC diagnosis of cancers. The probes can also be used to map the
 CC corresponding genomic sequence, while Ab are also useful in drug
 CC screening and for purifying native HCNB. Therapeutic agents are
 CC administered orally, intravenously, intramuscularly, topically or
 CC rectally, normally at 0.1-105 mu g.
 XX
 XX Sequence 191 AA:
 SO
 Query Match 96.8%; Score 875; DB 19; Length 191;
 Best local similarity 92.1%; Pred. No. 5,1e-79;
 Matches 176; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MGGSGSRLSKELLAEYODLFTLTKOELLAHRRFCLELPQEOITYESSLRACVPEOILS 60
 Db 1 MGGSSRSRLSKELLAEYODLFTLTKOELLAHRRFCLELPQEOITYESSLRACVPEOILS 60
 QY 61 LPELKANFKERICVFSTSPAKDLSFEDFLDLVSFSDTAPDKSHYAFRIFXXXXX 120
 Db 61 LPELKANFKERICVFSTSPAKDLSFEDFLDLVSFSDTAPDKSHYAFRIFXXXXX 120
 QY 121 XXXXXXXXSRVNCITGCEPTRLSASEMKQIDNILESDIDRGITNLSFQHYISRS 180
 Db 121 GTLNREDLSRLVNCITGCEPTRLSASEMKQIDNILESDIDRGITNLSFQHYISRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

DE Novel central nervous system protein #234.
 XX
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; anglogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 OS Homo sapiens.
 XX
 XX WO200155318-A2.
 XX PD 02-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01332.
 XX PR 31-JAN-2000; 2000US-0179065.
 XX PR 04-FEB-2000; 2000US-0180628.
 XX PR 24-FEB-2000; 2000US-0184664.
 XX PR 02-MAR-2000; 2000US-0186350.
 XX PR 16-MAR-2000; 2000US-0189874.
 XX PR 17-MAR-2000; 2000US-0190076.
 XX PR 18-APR-2000; 2000US-0198123.
 XX PR 07-JUN-2000; 2000US-0205515.
 XX PR 28-JUN-2000; 2000US-0209467.
 XX PR 30-JUN-2000; 2000US-0214886.
 XX PR 07-JUL-2000; 2000US-0215135.
 XX PR 07-JUL-2000; 2000US-0216647.
 XX PR 11-JUL-2000; 2000US-0216880.
 XX PR 11-JUL-2000; 2000US-0217487.
 XX PR 14-JUL-2000; 2000US-0218290.
 XX PR 26-JUL-2000; 2000US-0220963.
 XX PR 26-JUL-2000; 2000US-0220964.
 XX PR 14-AUG-2000; 2000US-0224518.
 XX PR 14-AUG-2000; 2000US-0224519.
 XX PR 14-AUG-2000; 2000US-0225213.
 XX PR 14-AUG-2000; 2000US-0225214.
 XX PR 14-AUG-2000; 2000US-0225266.
 XX PR 14-AUG-2000; 2000US-0225267.
 XX PR 14-AUG-2000; 2000US-0225268.
 XX PR 14-AUG-2000; 2000US-0225270.
 XX PR 14-AUG-2000; 2000US-0225447.
 XX PR 14-AUG-2000; 2000US-0225757.
 XX PR 14-AUG-2000; 2000US-0225758.
 XX PR 14-AUG-2000; 2000US-0225759.
 XX PR 18-AUG-2000; 2000US-0226279.
 XX PR 22-AUG-2000; 2000US-0226281.
 XX PR 22-AUG-2000; 2000US-0226285.
 XX PR 22-AUG-2000; 2000US-0226865.
 XX PR 22-AUG-2000; 2000US-0227182.
 XX PR 23-AUG-2000; 2000US-0227009.
 XX PR 30-AUG-2000; 2000US-0228924.
 XX PR 01-SEP-2000; 2000US-0229287.
 XX PR 01-SEP-2000; 2000US-0229343.
 XX PR 01-SEP-2000; 2000US-0229344.
 XX PR 01-SEP-2000; 2000US-0229345.
 XX PR 05-SEP-2000; 2000US-0229509.
 XX PR 05-SEP-2000; 2000US-0229513.
 XX PR 06-SEP-2000; 2000US-0230437.
 XX PR 06-SEP-2000; 2000US-0230438.
 XX PR 08-SEP-2000; 2000US-0231242.
 XX PR 08-SEP-2000; 2000US-0231243.
 XX PR 08-SEP-2000; 2000US-0231244.
 XX PR 08-SEP-2000; 2000US-0231413.
 XX PR 08-SEP-2000; 2000US-0231414.
 XX PR 08-SEP-2000; 2000US-0232080.
 XX PR 08-SEP-2000; 2000US-0232081.
 XX PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 FI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-581633/65.
 DR N-PSDB; ABK43654.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID No 842; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC ankylogeneses, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC
 Query Match 39.2%; Score 354; DB 22; Length 172;
 Best Local Similarity 40.7%; Pred. No. 8.5e-27;
 Matches 72; Conservative 44; Mismatches 51; Indels 10; Gaps 3;
 QY 13 LAEYODLFTLTKOETLLAHRRECELLPQORTVESSLRAQVPEQILSLPELKANPFKE 72
 Db 1 LEEYQALFTLRNEILCIHTLKLCPGKYKEATL----TMDQVSSLPALRVNFRDR 56
 QY 73 ICRVFSTSPAKDSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXXXXXSRV 132
 Db 57 ICRVFS---HKGMFSEFDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 113
 QY 133 NCLTGEGETRLSASEMKOLIDNILEESDITDRGTTNLSEFQHVSRSPDPFASFKI 189
 Db 114 LRLNSDD---MSEDLMLDNLNHLVSELDNDNMLSFSEFEHMAKSPDFMNSFRI 167
 RESULT 5
 AAM43562
 ID AAM43562 standard; Protein; 184 AA.
 XX
 AC AAM43562;
 XX
 DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 240.
DE
XX
KW Human; antirheumatic; antineumatic; antiproliferative; vasotropic;
KW Cerebroprotective; nootropic; neuroprotective; antibacterial; vitucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antinflammatory; antitumor; gene therapy; cancer; immune disorder;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
OS Homo sapiens.
XX
XX WO200155308-A2.
PN
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01309.
PF
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 08-SEP-2000; 2000US-0232081.
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PR 20-OCT-2000; 2000US-0241877.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0244676.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249247.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-488781/53.
DR N-PSDB; AAI63868.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
XX Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 184 AA;
SQ
Query Match 39.2%; Score 354; DB 22; Length 184;
Best Local Similarity 40.7%; Pred. No. 9.7e-27;
Matches 72; Conservative 44; Mismatches 51; Indels 10; Gaps 3;
QY 13 LAEYQDLTFLTKQETLLAHRFCCELLPQEQRTVESSLRAQVPEQILSLPELKANPFK 72
Db 13 LEEYQALTFELTRNEILCIHDTFLKCPGKYKEATL----TMDQVSSLPALRVNPFDR 68
QY 73 ICRVFTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXXXXXSRV 132
Db 69 ICRVFS---HKGMSFEDVLGMSVFEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 125
QY 133 NCLTGEEDTRLSASEMKQILNDINLEESDIDRGTINLSEFQHVISRSPDFASF 189
Db 126 LRLNSDD---MSEDLMLDNLHVLSDDLNDNMLSFSEFEHAKSPDFMNSFRI 179
RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX
XX AAB64418;
AC
XX
XX 22-MAR-2001 (first entry)
DT
XX
XX Amino acid sequence of human intracellular signalling molecule INTRA50.
DE
XX Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiarteriosclerotic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX
XX Homo sapiens.
OS
XX
XX W0200077040-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX 16-JUN-2000; 2000WO-US16636.
XX
XX 16-JUN-1999; 99US-0139566.
PR
XX 17-AUG-1999; 99US-0149840.
PR
XX 09-NOV-1999; 99US-0164417.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
XX
XX WPI; 2001-025334/03.
DR N-PSDB; AAF32687.
XX
XX New human intracellular signalling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX
XX Claim 5; Page 158-159; 192pp; English.
XX
XX Sequences AAF32638 - AAF32689 represent cDNA encoding human
CC intracellular signalling molecules INTRAL - INTRA52, represented in
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
CC of the invention exhibit immunosuppressive, cytostatic; neuroprotective;
CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
CC agonists and antagonists are useful for the treatment of a condition
CC associated with decreased or increased expression of functional INTRA.
CC Disorders associated with abnormal INTRA expression or activity include
CC cell proliferative disorders e.g. arteriosclerosis and cancers;
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections; gastrointestinal disorders e.g.
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
CC disorder. Antibodies immuno specific for the INTRA proteins may also be
CC useful in the diagnosis of the above disorders.
XX
XX Sequence 185 AA;
SQ
Query Match 38.9%; Score 352; DB 22; Length 185;
Best Local Similarity 40.8%; Pred. No. 1.5e-26;
Matches 73; Conservative 43; Mismatches 53; Indels 10; Gaps 3;
QY 11 ELLAEYQDLTFLTKQETLLAHRFCCELLPQEQRTVESSLRAQVPEQILSLPELKANPFK 70
Db 12 EDEEYQALTFELTRNEILCIHDTFLKCPGKYKEATL---TMDQVSSLPALRVNPFDR 67
QY 71 ERICRVFTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXXXXXSRV 130
Db 68 DRICRVFS---HKGMSFEDVLGMSVFEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 124
QY 131 LVNCLTGEEDTRLSASEMKQILNDINLEESDIDRGTINLSEFQHVISRSPDFASF 189
Db 125 IILRLNSDD---MSEDLMLDNLHVLSDDLNDNMLSFSEFEHAKSPDFMNSFRI 180
RESULT 7

AAE09736
 ID AAE09736 standard; Protein; 187 AA.
 XX
 AC AAE09736;
 XX
 DT 29-NOV-2001 (first entry)
 XX
 DE Human kinase interacting protein.
 XX
 KW Human; kinase interacting protein; novel human protein; NHP;
 KW gene therapy; drug screening; mental disorder; biological disorder;
 KW medical disease; neotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200166760-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 08-MAR-2001; 2001WO-US07499.
 XX
 PR 08-MAR-2000; 2000US-0187719.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Mathur B, Turner CA;
 XX
 DR WPI: 2001-557870/62.
 DR N-PSDB; AAD16796.
 XX
 PT Novel polynucleotides encoding human kinase interacting protein useful
 PT for drug screening, diagnosis and in gene therapy of biological
 PT disorders
 XX
 PS Claim 2; Page 31-32; 32pp; English.
 XX
 CC The present amino acid sequence is a novel human protein (NHP),
 CC human kinase interacting protein. NHP oligonucleotides are useful
 CC as hybridisation probes for screening libraries and assessing gene
 CC expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene are used to design primers for
 CC use in amplification assays to detect mutations within the exons,
 CC splice sites, introns that can be used in diagnostics and
 CC pharmacogenomics. NHP nucleotide sequences are useful for drug
 CC screening and nucleotide construct encoding NHP products are
 CC useful in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo.
 CC The encoded NHP polypeptides are useful for generating antibodies,
 CC as reagents in diagnostic assays, for identifying other cellular
 CC gene products related to NHP and as reagents in assays for screening
 CC for compounds that are useful in the treatment of mental, biological
 CC or medical disorders and diseases.
 XX
 SQ Sequence 187 AA;
 Query Match 37.2%; Score 336; DB 22; Length 187;
 Best Local Similarity 37.8%; Pred. No. 6.4e-25;
 Matches 73; Conservative 52; Mismatches 56; Indels 12; Gaps 5;

DB 173 ILRAPDLSTFHI 185
 RESULT 8
 ID ABB96054
 AC ABB96054 standard; Protein; 173 AA.
 XX
 AC ABB96054;
 XX
 DT 21-JUN-2002 (first entry)
 XX
 DE Human testicular antigen SEQ ID NO: 1438.
 XX
 KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
 KW reproductive system disorder; urinary system disorder; gene therapy;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disease; infection; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200155317-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01329.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220963.
 PR 14-AUG-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226281.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227189.
 PR 30-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229309.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.

XX
PA (HUMA-) HUMAN GENOME SCI INC

KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasia; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiotensin;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW

[illegible]

PD XX 05-JAN-2001; 2001US-0259678.
PF XX (HUMA-) HUMAN GENOME SCI INC.
XX XX Rosen CA, Barash SC, Ruben SM;
XX XX WPI; 2001-581633/65.
XX XX N-PSDB; ABR43942.
XX XX New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives -
, XX
PS Claim 9; SEQ ID NO 1130; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (III) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infection. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 36.3%; Score 328; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 3.5e-24;
Matches 69; Conservative 43; Mismatches 53; Indels 10; Gaps 3;
OY 13 LAEQDITFTKOBILLAHRRFCCLLPQEQRTVSSLRQVPPFQILSLKANPFKER 72
Db 1 LEEQALFTFLTRNEILCIHDTFLKCPGKYKATL----TMDQVSSLALRVNPFDR 56
OY 73 ICRVFSTPAKDSLFEDFLLSVSDTATPDIKSHYAFRIFXKXXXXXXXSRV 132
Db 57 ICRVFS---HKGMFSEFVLGMAVFSEQACPSLKIEYAFRIYDFNENGFIEDLQRII 113
OY 133 NCLTGEGETFLSASEMKQLIDNLEESDIDRGTINLSEFQVHSRDPFASFS 187
Db 114 LRLNSDD---MSEDLMLDTNRHVLXSDDLNDNMLSFSEFEHAKSPDFMTFF 165
RESULT 10
AAM95362
ID AAM95362 standard; Protein: 173 AA.
XX
AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX

PD XX 02-AUG-2001.
PF XX 17-JAN-2001; 2001WO-US01339.
XX XX 31-JAN-2000; 2000US-0179065.
XX XX 04-FEB-2000; 2000US-0180628.
XX XX 24-FEB-2000; 2000US-0184664.
XX XX 02-MAR-2000; 2000US-0186350.
XX XX 16-MAR-2000; 2000US-0189874.
XX XX 17-MAR-2000; 2000US-0190076.
XX XX 18-APR-2000; 2000US-0198123.
XX XX 19-MAY-2000; 2000US-0205515.
XX XX 07-JUN-2000; 2000US-0209467.
XX XX 28-JUN-2000; 2000US-0214886.
XX XX 30-JUN-2000; 2000US-0215135.
XX XX 07-JUL-2000; 2000US-0216647.
XX XX 11-JUL-2000; 2000US-0217487.
XX XX 11-JUL-2000; 2000US-0217496.
XX XX 14-JUL-2000; 2000US-0218290.
XX XX 26-JUL-2000; 2000US-0220963.
XX XX 26-JUL-2000; 2000US-0220964.
XX XX 14-AUG-2000; 2000US-0224518.
XX XX 14-AUG-2000; 2000US-0224519.
XX XX 14-AUG-2000; 2000US-0225213.
XX XX 14-AUG-2000; 2000US-0225214.
XX XX 14-AUG-2000; 2000US-0225266.
XX XX 14-AUG-2000; 2000US-0225267.
XX XX 14-AUG-2000; 2000US-0225268.
XX XX 14-AUG-2000; 2000US-0225270.
XX XX 14-AUG-2000; 2000US-0225447.
XX XX 14-AUG-2000; 2000US-0225757.
XX XX 14-AUG-2000; 2000US-0225758.
XX XX 18-AUG-2000; 2000US-0225759.
XX XX 22-AUG-2000; 2000US-0226681.
XX XX 22-AUG-2000; 2000US-0226868.
XX XX 22-AUG-2000; 2000US-0227182.
XX XX 23-AUG-2000; 2000US-0227009.
XX XX 30-AUG-2000; 2000US-0228924.
XX XX 01-SEP-2000; 2000US-0229287.
XX XX 01-SEP-2000; 2000US-0229343.
XX XX 01-SEP-2000; 2000US-0229344.
XX XX 05-SEP-2000; 2000US-0229345.
XX XX 05-SEP-2000; 2000US-0229509.
XX XX 05-SEP-2000; 2000US-0229513.
XX XX 06-SEP-2000; 2000US-0230437.
XX XX 08-SEP-2000; 2000US-0230438.
XX XX 08-SEP-2000; 2000US-0231242.
XX XX 08-SEP-2000; 2000US-0231243.
XX XX 08-SEP-2000; 2000US-0231244.
XX XX 08-SEP-2000; 2000US-0231413.
XX XX 08-SEP-2000; 2000US-0231414.
XX XX 08-SEP-2000; 2000US-0232080.
XX XX 08-SEP-2000; 2000US-0232081.
XX XX 12-SEP-2000; 2000US-0231968.
XX XX 14-SEP-2000; 2000US-0232397.
XX XX 14-SEP-2000; 2000US-0232398.
XX XX 14-SEP-2000; 2000US-0232399.
XX XX 14-SEP-2000; 2000US-0232400.
XX XX 14-SEP-2000; 2000US-0232401.
XX XX 14-SEP-2000; 2000US-0233063.
XX XX 14-SEP-2000; 2000US-0233064.
XX XX 14-SEP-2000; 2000US-0233065.
XX XX 21-SEP-2000; 2000US-0234223.
XX XX 21-SEP-2000; 2000US-0234274.
XX XX 25-SEP-2000; 2000US-0234997.
XX XX 25-SEP-2000; 2000US-0234998.
XX XX 26-SEP-2000; 2000US-0235484.
XX XX 27-SEP-2000; 2000US-0235834.
XX XX 27-SEP-2000; 2000US-0235836.
XX XX 29-SEP-2000; 2000US-0236327.
XX XX 29-SEP-2000; 2000US-0236367.

[illegible]

CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 173 AA;
Query Match 36.3%; Score 328; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 3,5e-24;
Matches 69; Conservative 43; Mismatches 53; Indels 10; Gaps 3;
QY 13 LAEYODLTFLLKQEIILAHRRFCELLPQEQRTVESLRQAVPFGQIISLPETKANPKER 72
Db 1 LEEYQALTFLLRNEILICHDFTLKCPGKYKRAATL---TMDQVSSLPALRYNPPDR 56
QY 73 ICAVFSTSPAKDSLSEDFIDLVSFSDTATPDIKSHYAFRIEYXXXXXXSRLV 132
Db 57 ICAVFSTSPAKDSLSEDFIDLVSFSDTATPDIKSHYAFRIEYXXXXXXSRLV 132
QY 133 NCLTGGEDTRLASSEKQIOLNILESDIDRGCTINLSEFQHYISRSPDPASSE 187
Db 114 LRLNSDD--MSEDLLMLTFNLVLSXSDLDNDNMLSFSEFEMAKSPDEMTPE 165
RESULT 12
AAU19952
ID AAU19952 standard; Protein: 173 AA.
XX AAU19952;
AC
XX
XX
DT 06-DEC-2001 (first entry)
XX
DE Novel human calcium-binding protein #61.
XX
XX Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiahrilic; cytosstatic; vasotropic; antibacterial; nootropic;
KW vincicite.
XX
XX Homo sapiens.
OS
XX
XX WO200155304-A2.
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01302.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218299.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 01-SEP-2000; 2000US-0229345.
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PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
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PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 26-SEP-2000; 2000US-0234584.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
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PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.

08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246609.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246613.
08-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249208.
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17-NOV-2000; 2000US-0249212.
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17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0255678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465568/50.
N-PSDB; AAS31637.
Isolated nucleic acid molecule encoding a calcium-binding protein is
used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID NO 149; 542pp; English.
The present invention relates to the isolation of novel human
calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
sequences encoding for these proteins. The sequences of the invention
are useful in the diagnosis, prevention and/or prognosis of diseases
associated with aberrant calcium flux. Such disorders include
neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
immune dysfunction (e.g. severe combined immunodeficiency, SCID),
digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
novel calcium-binding proteins are also useful as screening tools to
identify antagonists and/or agonists that may enhance or inhibit
activities mediated by calcium-binding proteins. The polynucleotides of
the invention are also useful in gene therapy. AAU9892-AAU19969
represent the novel human calcium-binding proteins.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 36.3%; Score 328; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 3.5e-24;
Matches 69; Conservative 43; Mismatches 53; Indels 10; Gaps 3;
QY 13 LAEQDITFLTKQIILLAHRRFCCELLPOEQRTVSSLRQVPPFQIILSPELKANPFKER 72
DB 1 LEEYQALTFLTRNEILCIHDTFLKCPGKYKATL-----TMDQVSLPALRVNPFDR 56
QY 73 ICRVFSTSPAKDSLFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXXXXXSRLV 132
DB 57 ICRVFS---HGMFSFEDVLGMSVSEQACPSLKIEAFRIYDFNENGFIDEEDLQRII 113
QY 133 NCLTGEGETRLSASEMKQLIDNILEESDDIDRGTINLSEFQHVISRSPDASSF 187
DB 114 LRLINSDD---MSRDLMLDLTNHVLXSXDLNDNMLSFSEFEHAMAKSPDFTMPF 165
RESULT 13
ABB64325.
ID ABB64325 standard; Protein; 206 AA.
XX ABB64325;
AC ABB64325;
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 19767.
DE Drosophila melanogaster polypeptide SEQ ID NO 19767.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
XX WO200171042-A2.
PD 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
PF 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL08428.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX Disclosure; SEQ ID NO 19767; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(AB857737-AB872072).
XX The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 206 AA;
QY 17 QDLTFLTKQIILLAHRRFCCELLPO---EQRTVSSLRQVPPFQIILSPELKANPFKERI 73
Query Match 35.5%; Score 320.5; DB 22; Length 206;
Best Local Similarity 40.9%; Pred. No. 2.8e-23;
Matches 72; Conservative 41; Mismatches 46; Indels 17; Gaps 5;


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DB      43 KCTFTRREILVHKKREFELRPDLVPMTEQASSVKKPCIEEMPELR----- 94
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DB      95 -EAFSND-CQGNISFEDFDLVSFSDTAPDLSKSHYAFIRFXKXXXXXXXXXXSLVN 149
OY      134 CTGEGEDTRLASSEMKOLIDNLESIDIDRGTINLSEFOHYISRSPDASFFKI 189
DB      150 CLFTMKK-ELSPENHOQIADKYEADVDGDKSLIFEFHYILRAPDLSFPHI 204

RESULT 14
ABP41194
ID      ABP41194 standard; Protein; 169 AA.
XX
AC      ABP41194;
XX
DT      23-AUG-2002 (first entry)
XX
DE      Human ovarian antigen HTLN94, SEQ ID NO:2326.
XX
KM      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KM      ovarian cancer; breast cancer; reproductive system disorder;
KM      infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KM      PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KM      inflammatory condition; immune disorder; blood disorder;
KM      cardiovascular disorder; respiratory disorder; neurological disorder;
KM      gastrointestinal disorder; urinary system disorder; drug screening;
KM      gene therapy; chromosome mapping; forensic analysis;
KM      antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KM      antiinflammatory; gynaecological; reproductive.
XX
OS      Homo sapiens.
XX
PN      WO200200677-A1.
XX
PD      03-JAN-2002.
XX
PF      07-JUN-2001; 2001WO-US18569.
XX
PR      07-JUN-2000; 2000US-209467P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Birse CE, Rosen CA;
XX
DR      WPI: 2002-147878/19.
XX
DR      N-PSDB; ABQ54271.
XX
PT      Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT      useful in the prevention, treatment and diagnosis of cancer (e.g.
PT      ovarian cancer), immune disorders, cardiovascular disorders and
PT      neurological diseases -
XX
PS      Claim 11; SEQ ID NO 2326; 2922pp; English.
XX
XX      The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX      ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX      encompasses polypeptides 904 identical and polynucleotides 954 identical
XX      to the sequences of the invention. The invention additionally relates to
XX      recombinant vectors and host cells comprising human ovarian antigen
XX      polynucleotides, antibodies against human ovarian antigens, and the use
XX      of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX      treating, prognosing or preventing various ovary and/or breast-related
XX      disorders. Such conditions include ovarian cancer and breast cancer, and
XX      metastatic tumours of ovarian or breast origin, reproductive system
XX      disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX      polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX      disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
XX      shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX      vaginitis), immune disorders (e.g., congenital and acquired
XX      immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

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CC      blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC      respiratory disorders, neurological disorders, gastrointestinal disorders
CC      and urinary system disorders. Ovarian antigen polypeptides and
CC      polynucleotides may also be used in screening for compounds which
CC      modulate ovarian antigen expression or activity. The polynucleotides may
CC      further be used for gene therapy, chromosome mapping, in the
CC      identification of individuals and in forensic analysis, and the
CC      polypeptides may be used as food additives or to prepare antibodies
CC      useful in disease diagnosis, drug targeting and phenotyping. The present
CC      sequence represents a human ovarian antigen of the invention.
CC      Note: The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence 169 AA:
XX
Query Match      24.9%; Score 225.5; DB 23; Length 169;
Best Local Similarity 33.3%; Pred. No. 6,5e-14;
Matches 42; Conservative 44; Mismatches 35; Indels 5; Gaps 2;

OY      64 LKANPFRERICRFPSTSPADSLFEDFDLVSFSDTAPDLSKSHYAFIRFXKXXXXX 123
DB      47 LQENPFRERIVAAFS-EDGEGLTFNDPDMFVSLCESAPREIKANYAFKIDFNTDNI 105
OY      124 XXXXXSRLVNCITGEGEDTRLASSEMKOLIDNLESIDIDRGTINLSEFOHYISRSPF 183
DB      106 CKEDLELTARL-----KSLDEBEVYLVCDKYEADVDGDKSLFAPDEDTAKAPDF 161
OY      184 ASSEFKI 189
DB      162 LSFPHI 167

RESULT 15
AA11976
ID      AA11976 standard; Protein; 120 AA.
XX
AC      AA11976;
XX
DT      18-JUN-1999 (first entry)
XX
DE      Human 5' EST secreted protein SEQ ID No: 576.
XX
KM      Human; secreted protein; EST; expressed sequence tag; diagnosis;
KM      forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KM      upstream regulatory sequence; cytokine activity; cell proliferation;
KM      differentiation; haematopoiesis regulation; tissue growth regulation;
KM      reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KM      thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS      Homo sapiens.
XX
PN      WO9906550-A2.
XX
PD      11-FEB-1999.
XX
PF      31-JUL-1998; 98WO-IB01232.
XX
PR      01-AUG-1997; 97US-0905144.
XX
PA      (GENS) GENSET.
XX
PI      Ducleert A, Dumas Milne Edwards J, Lacroix B;
XX
DR      WPI: 1999-153780/13.
XX
DR      N-PSDB; AAX40698.
XX
PT      New isolated prostate-derived nucleic acids - used to develop
PT      products which may have cytokine, immune regulatory, haematopoiesis
PT      regulating, anti-inflammatory or tumour inhibition activity
XX
PS      Claim 34; Page 664; 675pp; English.

```

CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate and encode the proteins
CC given in AAY11716 to AAY11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.

XX SQ Sequence 120 AA;

Query Match 24.0%; Score 217; DB 20; Length 120;

Best Local Similarity 100.0%; Pred. No. 2.4e-13;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGRLSKELLAEYQDLTFTKQELLHAHRCCELLPQQR 43

DB 1 MGGSGRLSKELLAEYQDLTFTKQELLHAHRCCELLPQQR 43

Search completed: January 17, 2003, 12:50:57

Job time : 36 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:50:20 ; Search time 15 Seconds

(Without alignments)
374.652 Million cell updates/sec

Title: US-09-878-454A-2X

904

Sequence: 1 MCGSGSRLSKELLAEYQDLT.....EFQWISRPDFASSFRIVL 191

Scoring table: BLOSUM62X

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5h_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6h_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6h_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	900	99.6	191	4	US-08-720-625-2
2	875	96.8	191	3	US-08-764-563-1
3	201.5	22.3	177	3	US-08-764-563-3
4	189.5	21.0	174	1	US-08-328-322-17
5	178.5	19.7	157	1	US-08-328-322-15
6	171.5	19.0	169	4	US-08-720-625-4
7	171.5	19.0	170	3	US-08-764-563-5
8	155.5	17.2	179	3	US-08-764-563-4
9	151	16.7	186	3	US-08-655-352-8
10	151	16.7	186	4	US-09-258-016-8
11	151	16.7	186	4	US-09-257-825B-8
12	135	14.9	193	3	US-08-655-352-3
13	135	14.9	193	4	US-09-257-825B-3
14	135	14.9	193	4	US-09-257-825B-7
15	133.5	14.8	196	3	US-08-655-352-4
16	126	13.9	220	4	US-09-399-913-26
17	126	13.9	220	4	US-09-298-731-26
18	125	13.8	191	3	US-08-655-352-7
19	125	13.8	191	4	US-09-257-825B-7
20	123	13.6	193	3	US-08-655-352-4
21	123	13.6	193	4	US-09-257-825B-4
22	123	13.6	193	4	US-09-257-825B-4
23	123	13.6	193	4	US-09-399-913-24
24	121	13.4	220	4	US-09-298-731-24
25	121	13.4	220	4	US-09-399-913-20
26	121	13.4	252	4	US-09-298-731-20
27	121	13.4	252	4	US-09-298-731-20

28	121	13.4	270	4	US-09-399-913-14	Sequence 14, Appl
29	121	13.4	270	4	US-09-298-731-14	Sequence 14, Appl
30	119.5	13.2	172	4	US-09-285-601-2	Sequence 2, Appl
31	119	13.2	193	3	US-08-655-352-2	Sequence 2, Appl
32	119	13.2	193	3	US-09-258-016-2	Sequence 2, Appl
33	118	13.1	193	4	US-09-257-825B-2	Sequence 2, Appl
34	118	13.1	270	4	US-09-399-913-18	Sequence 18, Appl
35	118	13.1	270	4	US-09-298-731-18	Sequence 18, Appl
36	116	12.8	216	4	US-09-399-913-6	Sequence 6, Appl
37	116	12.8	216	4	US-09-298-731-6	Sequence 6, Appl
38	116	12.8	225	4	US-09-399-913-30	Sequence 30, Appl
39	116	12.8	225	4	US-09-298-731-30	Sequence 30, Appl
40	116	12.8	227	4	US-09-399-913-8	Sequence 8, Appl
41	116	12.8	227	4	US-09-399-913-10	Sequence 10, Appl
42	116	12.8	227	4	US-09-298-731-8	Sequence 8, Appl
43	116	12.8	227	4	US-09-298-731-10	Sequence 10, Appl
44	116	12.8	245	4	US-09-399-913-4	Sequence 4, Appl
45	116	12.8	245	4	US-09-298-731-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gidson
STREET: P.O. Drawer 34009
City: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2
Query Match 99.6%; Score 900; DB 4; Length 191;
Best Local Similarity 92.7%; Pred. No. 1,1e-92;
Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGSGSRLSKELLAEYQDLTFLTKOELLAHRRFCCLLPQQRVSSSLRAQVFFQILS 60
Db 1 MCGSGSRLSKELLAEYQDLTFLTKOELLAHRRFCCLLPQQRVSSSLRAQVFFQILS 60
QY 61 LPELKNPFRERICRVPSTSPADSLSEFQDLISVFTQAPDIDKSHRAPIFXKXX 120
|||||
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Db 61 LPELKANPFKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFEDDD 120
QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREDLSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2
US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-08-764-563-1

Query Match 96.8%; Score 875; DB 3; Length 191;
Best Local Similarity 92.1%; Pred. No. 7e-90;
Matches 176; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPOEQRTVSSSLRAQVFFEQILS 60
Db 1 MGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPOEQRXESSLRAQVFFEQILS 60
QY 61 LPELKANPFKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXX 120
Db 61 LPELKANPFKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFDDDD 120
QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREDLSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 3
US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458230
; US-08-764-563-3

Query Match 22.3%; Score 201.5; DB 3; Length 177;
Best Local Similarity 26.4%; Pred. No. 4.4e-14;
Matches 47; Conservative 50; Mismatches 68; Indels 13; Gaps 3;
QY 1 MGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPOEQRTVSSSLRAQVFFEQILS 60
Db 1 MGTNTSSLRPEEVEEMQKGTNFTQKEIKKLYKRRKLDKDGNGTISK-----DEFLM 52
QY 61 LPELKANPFKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFXXXX 120
Db 53 IPELAVNPLVKRVISIPDEN-GGGSVNFKEFIAALSFNAGDKQRKLEFAKVVYDIDGD 111
QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIS 178
Db 112 GYISNGELFTVLKMWG----NNLSVQLQIQIVDKTILEADEDGDGKISFEFAKTLS 165
RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322

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      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/328,322
        FILING DATE: 24-Oct-1994
        CLASSIFICATION: 530
      ATTORNEY/AGENT INFORMATION:
        NAME: Sholtz, Charles K.
        REGISTRATION NUMBER: P38,615
        REFERENCE/DOCKET NUMBER: 8600-0151.10
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (415) 324-0880
        TELEFAX: (415) 324-0960
      INFORMATION FOR SEQ ID NO: 15:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 157 amino acids
          TYPE: amino acid
          TOPOLOGY: linear
        MOLECULE TYPE: protein
      US-08-328-322-15

Query Match              19.7%; Score 178.5; DB 1; Length 157;
Best Local Similarity    24.0%; Pred. No. 1,3e-11;
Matches 37; Conservative 50; Mismatches 54; Indels 13; Gaps 3;

QY   24 KOELLHARRPCCELLPQORTVESSLRAQVFEQILSLPELKANPFKERICRVSTSPAK 83
     | :|::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db   3 RDEITERLRKRMKIDRPSGSGSIDKN-----EFMSIPGVSNPLAGRIIMEVFADNDSR 54
QY   84 DSLSEFDIEDLSVESPTATPDIKSHYAIFRIEXXXXXXXXSLRYNCITTEGEDTR 143
     |:|::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db   55 D-VFOEETIGLSTFGSGSKDEKLRAFKEYIDDKGFISNGELFTYLKIMVG----SN 109
QY   144 LSASEMKQLDNIIEESDIDRDGTINTSEFOHWI 177
     |:|::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db   110 LDDEQLQIVDRITVENDDSDGRSLSEEPFNMAI 143

RESULT 6
US-08-720-625-4
: Sequence 4, Application US/08720625
: Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: NC. 6242587Ch Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-720-625-4

Query Match 19.0%; Score 171.5; DB 4; Length 169;
Best Local Similarity 27.0%; Pred. No. 9.5e-11;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKRICRVFSTSPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 115
DB 40 EEFMSLPELQNPVQRVIDIFDITD-GNCEVDKFEFIEGVSVKGDKEOKLRFARIY 98

QY 116 XXXXXXXXXXXXSLVNCVTGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOH 175
DB 99 DMDKGYISNGELFQVLKMWG-----NNLKDTQLQOIVDKTIINADKGDGRISFEFCA 154

QY 176 VI 177
DB 155 VV 156

RESULT 7
US-08-764-563-5
; Sequence 5, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 461682
US-08-764-563-5

Query Match 19.0%; Score 171.5; DB 3; Length 170;

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Best Local Similarity 27.0%; Pred. No. 9.7e-11;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKRICRVFSTSPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 115
DB 41 EEFMSLPELQNPVQRVIDIFDITD-GNCEVDKFEFIEGVSVKGDKEOKLRFARIY 99

QY 116 XXXXXXXXXXXXSLVNCVTGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOH 175
DB 100 DMDKGYISNGELFQVLKMWG-----NNLKDTQLQOIVDKTIINADKGDGRISFEFCA 155

QY 176 VI 177
DB 156 VV 157

RESULT 8
US-08-764-563-4
; Sequence 4, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 109612
US-08-764-563-4

Query Match 17.2%; Score 155.5; DB 3; Length 179;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
Matches 37; Conservative 39; Mismatches 62; Indels 13; Gaps 3;

QY 35 CELLPQEQ-----RTVESSLRAQVPEQILSLPELKANPFKRICRVFSTSPAKDSL 86
DB 12 CNHFDQEEIRRLGKFRKLDKSGSLSTEFPWRLPELOQNPLVGRVIDIFDITD-GNGEV 70

QY 87 SPEDFDLLSVFSDTATPDIKSHYAFRIXXXXXXXXXXXXXXXXXSLVNCVTGEGEDTRL 146

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Db 71 DHEHIVTSOPSVKGDDEQKLEAFRIYDMNDGFIENGELQVLMKMWG----NNLKD 126
QY 147 SEMKOLINILESDIDRGTINLSEFOHVI 177
Db 127 WQLOQVDSKSLVLDKDGDRISFEESDV 157

RESULT 9
US-08-655-352-8

Sequence 8, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhinua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequen
DESCRIPTION: (Gen2:Diofreq) with homology to 111y
DESCRIPTION: CCAMK
US-08-655-352-8

Query Match 16.7%; Score 151; DB 3; Length 186;
Best Local Similarity 22.3%; Pred. No. 2.4e-08;
Matches 44; Conservative 49; Mismatches 82; Indels 22; Gaps 5;
QY 1 MGSGSRLSKELAEYQDLTFLKOEILAHRRFCCLLPQEQTVSSSLRAQVFFQILS 60
Db 1 MGKSSKSLKQDITDLRTTFTTEKIRQNHKGFLKDCPGLLTEGQFIYKQF----- 55
QY 61 LPELKAPFERICRYVSTSPAKDSLFEEDLDLVSFDPATPDIKSHYAFRIFFXXXXX 120
Db 56 FPGQDPSKFSALYFVFDEN-NDGSLFEFEFIALSVTSKGL--DEKQMAFLYDVND 112
QY 121 XXXXXXXXSLVNCV-----TGEGEDTRLSASEMKOLINILESDIDRGTINLSE 172
Db 113 GYITREMNINIVDAIYQWGOQPOSEDEMT-----PKRVKXIFPQMKNHGKLTLEE 166

QY 173 FOHVISRSPDFASSFKI 189
Db 167 FREGSKADPRIVQALSL 183

RESULT 10
US-09-258-016-8

Sequence 8, Application US/09258016
Patent No. 6362395
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhinua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequen
DESCRIPTION: (Gen2:Diofreq) with homology to 111y
DESCRIPTION: CCAMK
US-09-258-016-8

Query Match 16.7%; Score 151; DB 4; Length 186;
Best Local Similarity 22.3%; Pred. No. 2.4e-08;
Matches 44; Conservative 49; Mismatches 82; Indels 22; Gaps 5;
QY 1 MGSGSRLSKELAEYQDLTFLKOEILAHRRFCCLLPQEQTVSSSLRAQVFFQILS 60
Db 1 MGKSSKSLKQDITDLRTTFTTEKIRQNHKGFLKDCPGLLTEGQFIYKQF----- 55
QY 61 LPELKAPFERICRYVSTSPAKDSLFEEDLDLVSFDPATPDIKSHYAFRIFFXXXXX 120
Db 56 FPGQDPSKFSALYFVFDEN-NDGSLFEFEFIALSVTSKGL--DEKQMAFLYDVND 112
QY 121 XXXXXXXXSLVNCV-----TGEGEDTRLSASEMKOLINILESDIDRGTINLSE 172
Db 113 GYITREMNINIVDAIYQWGOQPOSEDEMT-----PKRVKXIFPQMKNHGKLTLEE 166
QY 173 FOHVISRSPDFASSFKI 189
Db 167 FREGSKADPRIVQALSL 183

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RESULT 11
US-09-257-825B-8
; Sequence 8, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila
US-09-257-825B-8

Query Match 16.7%; Score 151; DB 4; Length 186;
Best Local Similarity 22.3%; Pred. No. 2.4e-08;
Matches 44; Conservative 49; Mismatches 82; Indels 22; Gaps 5;

QY 1 MGGSGRSLKELLAEYQDITFTLTKQBIILAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
DB 1 MGKSKLKQDITDRUTDTYTEREIROWHKGFLKDCPNGLLTGEGFKIKYQF----- 55
QY 61 LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXX 120
DB 56 FPGQDSKASLVFRYFDEN-NDGSIETEFIRALSVTSGKL--DEKLQWAFRLYDVND 112
QY 121 XXXXXXXXSLVNL-----TGGEOTRLSASEMKOLIDNILESDIDRDGTINLSE 172
DB 113 GYITREEMNIVDAIQVMVQQPQSEDENT-----PQRVDKIFQDMKNHDKGLTLEE 166
QY 173 FQVHSRSPDFASSFKI 189
DB 167 FREGSKADPRIVQALS 183

RESULT 12
US-08-655-352-3
; Sequence 3, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:

```

```

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 228-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural visinin-like protein
DESCRIPTION: (Gen2:Ratnvp3) with homology to lily
DESCRIPTION: CCaMK
US-08-655-352-3

Query Match 14.9%; Score 135; DB 3; Length 193;
Best Local Similarity 22.6%; Pred. No. 1.6e-06;
Matches 47; Conservative 50; Mismatches 75; Indels 36; Gaps 7;

QY 1 MGGSGRSLKELLAEYQDITFTLTKQBIILAHRRFCELLPQEQRTVSSLRQAQVPEQILS 60
DB 1 MGKSKLKQDITDRUTDTYTEREIROWHKGFLKDCPNGLLTGEGFKIKYQF-----FKKIYA 53
QY 61 --LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXX 118
DB 54 NFFPGDASKFAHVFRTDIN-SGDTIDRFRIALSVTSGKL--DEKLQWAFRLYDVND 111
QY 119 XXXXXXXXSLVNL-----TGGEOTRLSASEMKOLIDNILESDIDRDGTIN 169
DB 112 GNGYLSRSEMELVQAI-----YKMSVSMKMPEDSTPEKRTDKIFROMDINNDGKLS 165
QY 170 LSEF-----QHVHSRSPDFASSF 187
DB 166 LEEFKGAKSDPSIVRLQLQDPSSASQF 193

RESULT 13
US-09-258-016-3
; Sequence 3, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```


NAME: Stephens Jr., Donald L.
 REGISTRATION NUMBER: 34,022
 REFERENCE/DOCKET NUMBER: 4630-51994
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 DESCRIPTION: Region of rat neural visinin-like protein
 (Gen2:Ratnvp3) with homology to 11ly
 DESCRIPTION: CCAMK
 US-09-258-016-3

Query Match 14.9%; Score 135; DB 4; Length 193;
 Best Local Similarity 22.6%; Pred. No. 1.6e-06;
 Matches 47; Conservative 50; Mismatches 75; Indels 36; Gaps 7;

QY 1 MGSSGSLKELLAEYODLFTLKOEILLAHRRFCCLLPQEQRTVSSSLRAQVPEQILS 60
 DB 1 MGKONSKLPEVLDLREHTEFDHLEQWKGLKDCPTGHLTVDE-----FKKIYA 53
 QY 61 --LPELKNPKERICRVSTSPAKDSLPEDFLDLSVPSDTATPDIKSHYAFRIPIXXX 118
 DB 54 NFFPYGDASKFAEHVFRITDIN-SDGTIDPREFIILSVTS-RGKLEQKIKMAFPMYDLD 111
 QY 119 XXXXXXXXXXSLVNCILTEGEGEDTRLASSEM-----QLIDNILESDIDRDGTIN 169
 DB 112 GNGYISRSEMLEIVQAI-----YKMWSSVMKKPDESDPEKRTDIFRQMDINNDCKLS 165
 QY 170 LSEF-----QHVISRSPDFASSF 187
 DB 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 14

US-09-257-825B-3
 Sequence 3, Application US/09257825B
 Patent No. 6403352
 GENERAL INFORMATION:
 APPLICANT: Poovaiiah, Bachettira W.
 APPLICANT: Patil, Shameekumar
 APPLICANT: Takezawa, Daisuke
 TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
 FILE REFERENCE: 4630-51993
 CURRENT APPLICATION NUMBER: US/09/257,825B
 PRIOR FILING DATE: 1999-02-25
 PRIOR APPLICATION NUMBER: US 08/655,352
 PRIOR FILING DATE: 1996-05-23
 PRIOR APPLICATION NUMBER: US 60/014,743
 PRIOR FILING DATE: 1996-03-28
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Rat
 US-09-257-825B-3

Query Match 14.9%; Score 135; DB 4; Length 193;
 Best Local Similarity 22.6%; Pred. No. 1.6e-06;
 Matches 47; Conservative 50; Mismatches 75; Indels 36; Gaps 7;

QY 1 MGSSGSLKELLAEYODLFTLKOEILLAHRRFCCLLPQEQRTVSSSLRAQVPEQILS 60
 DB 1 MGKONSKLPEVLDLREHTEFDHLEQWKGLKDCPTGHLTVDE-----FKKIYA 53
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QY 119 XXXXXXXXXXSLVNCILTEGEGEDTRLASEMK-----QLIDNILESDIDRDGTIN 169
 DB 112 GNGYISRSEMLEIVQAI-----YKMWSSVMKKPDESDPEKRTDIFRQMDINNDCKLS 165
 QY 170 LSEF-----QHVISRSPDFASSF 187
 DB 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 15

US-09-048-889-1
 Sequence 1, Application US/09048889
 Patent No. 6117989
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl J.
 APPLICANT: Lai, Preeti
 TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/048,889
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cetrone, Michael C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PF-0493 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 196 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: COLNOT09
 CLONE: 1846517
 US-09-048-889-1

Query Match 14.8%; Score 133.5; DB 3; Length 196;
 Best Local Similarity 20.6%; Pred. No. 2.5e-06;
 Matches 39; Conservative 48; Mismatches 69; Indels 33; Gaps 6;

QY 5 GSRLSKELLAEYODLFTLKOEILLAHRRFCCLLPQEQRTVSSSLRAQVPEQILS 60
 DB 2 GSRTSAAVYIPDGSIRRETGFSQASLLRLHRR-----RALDRNKKGYLSRNDLQ 53
 QY 61 LPELKNPKERICRVSTSPAKDSLPEDFLDLSV-----STAPPDITS----- 108
 DB 54 ICALAVNPLGDKRTISFPG-GSQRVDFGFAVLAHFRVDEDETEQDPKKPEPLNSR 112

QY 109 ----HYAFRIXXXXXXXXXXSRVNCITGEGEDTRLSASEMKOLIDNILESDIDR 164
Db 113 RNLHIAFQLYLDRODKISRHEMLQVLRMLVG-----VQVTEEQENIADRTVQEADEG 168
QY 165 DGTINLSEF 173
Db 169 DGAVSFVEF 177

Search completed: January 17, 2003, 12:52:39
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:51:00 (Search time 11 Seconds
(without alignments)
345.163 Million cell updates/sec

Title: US-09-878-454a-2x

Perfect score: 904
Sequence: 1 MCGSGSRSLKELAEYODLT.....EFOHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	904	100.0	191	10	US-09-878-454a-2
2	892	98.7	191	12	US-10-109-885-2
3	336	37.2	187	10	US-09-802-116-2
4	171.5	19.0	170	12	US-10-109-885-3
5	161.5	17.9	195	10	US-09-999-602-3
6	157.5	17.4	195	10	US-09-999-602-4
7	134	13.9	214	10	US-09-999-602-1
8	126	13.8	220	10	US-09-350-874-26
9	121	13.4	220	10	US-09-350-874-24
10	121	13.4	252	10	US-09-350-874-20
11	121	13.4	270	10	US-09-350-874-14
12	118	13.1	216	10	US-09-350-874-6
13	116	12.8	225	10	US-09-350-874-30
14	116	12.8	227	10	US-09-350-874-8
15	116	12.8	227	10	US-09-350-874-10
16	116	12.8	245	10	US-09-350-874-4
17	116	12.8	252	10	US-09-350-874-22
18	116	12.8	252	10	US-09-350-874-22
19	116	12.8	252	10	US-09-350-874-22

20	116	12.8	252	10	US-09-350-874-42	Sequence 42, Appl
21	116	12.8	257	10	US-09-350-874-16	Sequence 16, Appl
22	115	12.7	216	9	US-09-965-528-15	Sequence 15, Appl
23	115	12.7	216	10	US-09-350-874-2	Sequence 2, Appl
24	107	11.8	229	10	US-09-350-874-70	Sequence 70, Appl
25	107	11.8	233	10	US-09-350-874-49	Sequence 49, Appl
26	107	11.8	250	10	US-09-350-874-72	Sequence 72, Appl
27	104.5	11.6	142	10	US-09-910-071-4	Sequence 4, Appl
28	104.5	11.6	172	12	US-10-109-885-4	Sequence 2, Appl
29	103	11.4	642	9	US-09-554-000-2	Sequence 6, Appl
30	103	11.4	642	9	US-09-554-000-6	Sequence 4, Appl
31	103	11.4	652	9	US-09-554-000-4	Sequence 5, Appl
32	103	11.4	656	9	US-09-554-000-8	Sequence 692, App
33	97.5	10.8	159	10	US-09-910-071-5	Sequence 8, Appl
34	96.5	10.7	1210	10	US-09-922-217-692	Sequence 692, App
35	96.5	10.7	1210	10	US-09-922-217-692	Sequence 1095, Ap
36	96.5	10.7	1210	10	US-09-833-263-692	Sequence 714, App
37	96.5	10.7	1548	9	US-10-025-380-1095	Sequence 32, Appl
38	96.5	10.7	1548	10	US-09-922-217-1095	Sequence 1095, Ap
39	96	10.6	256	10	US-09-350-874-32	Sequence 36, Appl
40	94.5	10.5	201	10	US-09-925-297-714	Sequence 34608, A
41	92	10.2	256	10	US-09-350-874-36	Sequence 5229, A
42	91.5	10.1	139	10	US-09-864-761-34808	Sequence 12125, A
43	91.5	10.1	1184	10	US-09-815-242-5229	Sequence 82, Appl
44	91.5	10.1	1188	10	US-09-815-242-12125	
45	91	10.1	330	9	US-09-870-759-82	

ALIGNMENTS

RESULT 1
US-09-878-454a-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Monteliro, et al.
TITLE OF INVENTION: Method of controlling the binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454a-2

Query Match 100.0%, Score 904, DB 10, Length 191,
Best Local Similarity 93.2%, Pred. No. 2.9e-78;
Matches 178; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGSGSRSLKELAEYODLTFLTKOETILAHRFCELLPOEORTYESSIRAAVPEQILS 60
DB 1 MCGSGSRSLKELAEYODLTFLTKOETILAHRFCELLPOEORTYESSIRAAVPEQILS 60
QY 61 LPELKNPKEKICRVFSTSPAKDSLSEDFDLILSVSDTATPDIKSHYARIRYXXXX 120
DB 61 LPELKNPKEKICRVFSTSPAKDSLSEDFDLILSVSDTATPDIKSHYARIRYXXXX 120
QY 121 XXXXXXXXSLVNCITGEGEDRLTASAEKKOLINDILESDIDRGTINLSEFOVIRS 180
DB 121 GLLNEDSLRLVNCITGEGEDRLTASAEKKOLINDILESDIDRGTINLSEFOVIRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191
RESULT 2

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US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match 98.7%; Score 892; DB 12; Length 191;
Best Local Similarity 92.1%; Pred. No. 4e-77;
Matches 176; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MGGSGRLSKELLAYQDLTLTKQELLAAHRRFCCELLPQRTVSSSLRAQVPFEQILS 60
QY 61 LPELANPFKERICRVSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXX 120
DB 61 LPELANPFKERICRVSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDDDD 120
QY 121 XXXXXXSLVNCITGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIRS 180
DB 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020082406A1 Human Kinase Interacting Protein and Polype
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match 37.2%; Score 336; DB 10; Length 187;
Best Local Similarity 37.8%; Pred. No. 3.1e-24;
Matches 73; Conservative 52; Mismatches 56; Indels 12; Gaps 5;

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QY 1 MGGSGRLSKELLAYQDLTLTKQELLAAHRRFCCELLPQRTVSSSLRAQVPFE 56
DB 1 MGNKQTVFTHEQLEAYQDCTFTTKEIMRLFRYQDLAPQLVPLDYTTCPD---VKVPYE 57
QY 57 QILSLPELKANPFKERICRVSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFX 116
DB 58 LIGSMPELKANPFKORIAQVFS-EDGDGHMTLDNFDLWFSWSENAAPDLKAYIAFKIYD 116
QY 117 XXXXXXSLVNCITGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176
DB 117 FNDDYICAWDLEQTVTKLT-RGE---LSAEVSLVCKVLDEADGDHGRSLSEDFQNM 172
QY 177 ISRSPDFASSFKI 189
DB 173 ILRAPDFLSTPHI 185

RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match 19.0%; Score 171.5; DB 12; Length 170;
Best Local Similarity 27.0%; Pred. No. 1.1e-08;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIF 115
DB 41 EEFNSLPELQNPVQVRVIDFTD-GNCEVDFKEFIEGVQSVKGDKEQLRPAFRIV 99
QY 116 XXXXXXSLVNCITGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 175
DB 100 DMDKDYISNGELFQVLKMAVG---NNLKDQLQQLIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 WV 157

RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

```

```

CURRENT APPLICATION NUMBER: US/09/999,602
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/010,378
PRIOR FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020091084A1 g1226242
US-09-999-602-3

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```

Query Match      17.9% Score 161.5; DB 10; Length 195;
Best Local Similarity 24.1%; Pred. No. 1.3e-07;
Matches 47; Conservative 45; Mismatches 74; Indels 29; Gaps 6;

```

```

QY 1 MGGSGSRLSK-ELLAEXODLFLTKOEILLAHRRFCELLPOEQRTVSSLRAGVPEQIL 59
DB 1 MGGSRATLLRDELLEIKKTGSHSQITLYSRFTSLDKGNGTISR-----EDFQ 52
QY 60 SLPKAMPFKERICRVFSTSPAKDSLSFEDFLDLISVF-----SDTAPPD----- 105
DB 53 RIPELAINPLGRIINAF-FSEGEDQVNFGRFMTLAHFRPIEDNEKSKDVNGPEPLNSR 111
QY 106 -IKSHAFRLFXXXXXXXXXXSRVNLCTGEGEDTRLASSEMQLDNIIEESDIDR 164
DB 112 SNKLHFAFLYLDKDKDKISRDQLVLRMVG-----VNISDQLGSIADRTIOEADQDG 167
QY 165 DGTINLSEFOHVISR 179
DB 168 DSAISTFEFVKVLEK 182

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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/09999602
; Patent No. US30020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1706967
US-09-999-602-4

```

```

Query Match      17.4% Score 157.5; DB 10; Length 195;
Best Local Similarity 23.6%; Pred. No. 3.2e-07;
Matches 46; Conservative 45; Mismatches 75; Indels 29; Gaps 6;

```

```

QY 1 MGGSGSRLSK-ELLAEXODLFLTKOEILLAHRRFCELLPOEQRTVSSLRAGVPEQIL 59
DB 1 MGGSRATLLRDELLEIKKTGSHSQITLYSRFTSLDKGNGTISR-----EDFQ 52
QY 60 SLPKAMPFKERICRVFSTSPAKDSLSFEDFLDLISVF-----SDTAPPD----- 105
DB 53 RIPELAINPLGRIINAF-FSEGEDQVNFGRFMTLAHFRPIEDNEKSKDVNGPEPLNSR 111

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QY 106 -IKSHAFRLFXXXXXXXXXXSRVNLCTGEGEDTRLASSEMQLDNIIEESDIDR 164
DB 112 SNKLHFAFLYLDKDKDKISRDQLVLRMVG-----VNISDQLGSIADRTIOEADQDG 167
QY 165 DGTINLSEFOHVISR 179
DB 168 DSAISTFEFVKVLEK 182

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RESULT 7
US-09-999-602-1
; Sequence 1, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 134682
US-09-999-602-1

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```

Query Match      14.8% Score 134; DB 10; Length 214;
Best Local Similarity 22.7%; Pred. No. 6.5e-05;
Matches 42; Conservative 39; Mismatches 50; Indels 54; Gaps 6;

```

```

QY 1 MGGSGSRLSK-ELLAEXODLFLTKOEILLAHRRFCELLPOEQRTVSSLRAGVPEQIL 59
DB 1 MGAHS--ASEEVRLEKGTGFSDDIEQLHRRF-KQLSDQDTIRK-----ENFNN 49
QY 61 LPELKAMPFKERICRVF-----STPAKDSLSFEDFLDLISVSDTAPPDPIKSHYAF 112
DB 50 VPDLEINPIRSKIVRAFFEDNRNLRKPGSGIADENFEDFTINSYF----- 96
QY 113 RIFXXXXXXXXXXSRVNLCTGEGEDTRLASSEMQLDNIIEESDIDRGTINLSE 172
DB 97 ---PIDTMDDEOVLELS-----KEKIRLFHMYDSDSGRTTLEE 134
QY 173 FOHVI 177
DB 135 YRNVV 139

```

```

RESULT 8
US-09-350-874-26
; Sequence 26, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenglian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731

```



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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-14

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Query Match	13.4%;	Score 121;	DB 10;	Length 270;
Best Local Similarity	20.7%;	Pred. No. 0.0017;		
Matches	38;	Conservative	55;	Mismatches 77;
			Indels	14;
			Gaps	5

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0Y      11 ELAEYODLFTLTCOEILLARRECELLPOQORVVESTSLRAQVFEOLLS-LPELKANP 68
Db      91 EGLELOEQOTFTFKRELOVLYRGFKNECP-----GVIYNEENFKQIYSQFFPGQSDST 143
QY      69 FKERICRFTSPSPAKDLSFEDF*LDLVSFSDATPDKSHYARIRPXXXXXXXXXXXXX 128
Db      144 YATLEFNAPFDIN-HDGSVSFEDFVAGISVYL-RGTVDRLMANNLTLDLNKGDTYKHEM 201
QY      129 SRLVNC--LTVGEGEDTRLASSEKKOLIDNILEESDIDRGTILISEFOHYISRPFPAS 185
Db      202 LDINKSTYDMGKTYTPALRREAPAREHVESFQAMDNKKQGVATIEEFTISCQKDEYIMR 261

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Qy	186	SFKI	189
		::	
Db	262	SMQL	265

RESULT 12
US-09-350-874-18
; Sequence 18, Application US/09350874
; Patent No. US20020019020A1

```

1  TITLE OR INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
2  FILE REFERENCE: NMI-069
3  CURRENT APPLICATION NUMBER: US/09/350,874
4  CURRENT FILING DATE: 1999-07-09
5  EARLIER APPLICATION NUMBER: USSN 60/110,277
6  EARLIER FILING DATE: 1998-11-30
7  EARLIER APPLICATION NUMBER: USSN 60/110,033
8  EARLIER FILING DATE: 1998-11-25
9  EARLIER APPLICATION NUMBER: USSN 60/109,333
10 EARLIER FILING DATE: 1998-11-20
11 EARLIER APPLICATION NUMBER: USSN 09/298,731
12 EARLIER FILING DATE: 1999-04-23
13 NUMBER OF SEQ ID NOS: 72
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ ID NO 18
16 LENGTH: 270
17 TYPE: PR1
18 ORGANISM: Mus musculus
19 US-09-350-874-18

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Query Match	13.1%	Score 118;	DB 10;	Length 270;
Best Local Similarity	22.0%	Pred. No. 0.0033;		
Matches	37;	Conservative	51;	Mismatches 66;
			Indels	14;
			Gaps	5

[illegible]

```

QY      129  SRLVNC---LTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEF 173
      ::  |  ::  |  ::  |  ::  |  ::  |  ::  |  ::  |  ::  |
Db      202  LDIMKSIYDMGKYYTPALREAPREHVESFQKMDRNKDGVTITLSEF 249

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RESULT 13

US-09-350-874-6
; Sequence 6, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION.

```

; TITLE INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
;
; FILE REFERENCE: NMI-069
;
; CURRENT APPLICATION NUMBER: US/09/350,874
;
; EARLIER FILING DATE: 1999-07-09
;
; EARLIER APPLICATION NUMBER: USSN 60/110,277
;
; EARLIER FILING DATE: 1998-11-30
;
; EARLIER APPLICATION NUMBER: USSN 60/110,033
;
; EARLIER FILING DATE: 1998-11-25
;
; EARLIER APPLICATION NUMBER: USSN 60/109,333
;
; EARLIER FILING DATE: 1998-11-20
;
; EARLIER APPLICATION NUMBER: USSN 09/298,731
;
; EARLIER FILING DATE: 1999-04-23
;
; NUMBER OF SEQ ID NOS: 72
;
; SOFTWARE: PatentIn Ver. 2.0

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```

; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-6

```

Query Match	12.8%	Score 116;	DB 10;	Length 216;
Best Local Similarity	22.6%;	Pred. No. 0.0034;		
Matches 38;	Conservative 43;	Mismatches 73;	Indels 14;	Gaps 5;

QY 11 ELLEFYODLFRTLOELLIAHRRCELLPOQKRVESLRQVFEOLTS--LPELKANP 68
Db 37 EGLEQLLAQNTFRTRELQVLYRGFKNCP-----SGVNEETFKQIYAQFFPHGADST 89
QY 69 FKERICAEVSTSPAKDSLSEFDEFLDLSVSDATPTPIKSHYARIRFXXXXXXXXXXXXX 120
Db 90 YAHLEFNAAFDTQT--GSVKEDFETALSTILL--RGTVERKLRMTFNLNLDINKDGYINKEEM 147
QY 129 SRLVNC---LTGEGEDFRLSASEKQOLIDNILEESDIDDOGTINUSEF 173
Db 148 MDIYKALAYDMAGKTYTPVKLEDPTROAVDVFQMKDKKKDSIYVLDEF 195

RESULT 14
US-09-350-874-30
; Sequence 30, Application US/09350874
; Patent No. US20020019020A1

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? TITLE OR INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
?
? FILE REFERENCE: MNI-069
?
? CURRENT APPLICATION NUMBER: US/09/350,874
?
? EARLIER FILING DATE: 1999-07-09
?
? EARLIER APPLICATION NUMBER: US98 60/110,277
?
? EARLIER FILING DATE: 1998-11-30
?
? EARLIER APPLICATION NUMBER: US98 60/110,033
?
? EARLIER FILING DATE: 1998-11-25
?
? EARLIER APPLICATION NUMBER: US98 60/109,333
?
? EARLIER FILING DATE: 1998-11-20
?
? EARLIER APPLICATION NUMBER: US98 09/298,731
?
? EARLIER FILING DATE: 1999-04-23
?
? NUMBER OF SEQ ID NOS: 72
?
? SOFTWARE: PatentIn Ver. 2.0

```

```

; TYPE: PRT
; ORGANISM: Rattus sp
US-09-350-874-30

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Query Match	12.8%;	Score 116;	DB 10;	Length 225;
Best Local Similarity	22.0%;	Pred. No. 0.0037;		
Matches 37;	Conservative 50;	Mismatches 67;	Indels 14;	Gaps 5;

Search completed: January 17, 2003, 12:52:57
Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:50:00 ; Search time 16 seconds

(without alignments)
1147.605 Million cell updates/sec

Title: US-09-878-454a-2x

Sequence score: 904

Sequence: 1 MGGSGSRLSKELLAEYDLT.....EFQHVISRSPDFASSPKIYL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	43.5	311	2	T21563 hypothetical prote
2	196.5	21.7	174	2	T41632 probable calcineur
3	189.5	21.0	175	2	JH0462 phosphoprotein pho
4	185.5	20.5	174	2	T47245 calcineurin regula
5	171.5	19.0	170	1	A33391 calcineurin regula
6	171.5	19.0	170	1	S34127 calcineurin regula
7	171.5	19.0	170	1	UC1220 calcineurin regula
8	171.5	19.0	170	1	S42716 calcineurin regula
9	169.5	18.8	369	2	T22708 calcineurin regula
10	165.5	18.3	195	2	T28047 hypothetical prote
11	164.5	18.2	213	2	T31775 hypothetical prote
12	161.5	17.9	170	2	JC5174 calcineurin regula
13	160.5	17.8	170	2	UC7242 calcineurin regula
14	157.5	17.4	170	2	A4307 calcineurin regula
15	156.5	17.3	226	2	T51357 calcineurin regula
16	155.5	17.2	179	2	JC1221 calcineurin regula
17	153.5	17.0	165	2	P50261 calcineurin regula
18	153.5	17.0	176	2	J01232 calcineurin regula
19	148.5	16.4	190	2	T20725 calcineurin regula
20	146	16.2	192	2	T01375 calcium sensor hom
21	144.5	16.0	226	2	T08923 calcineurin B-like
22	142	15.7	246	2	T05308 hypothetical prote
23	142	15.7	246	2	H85387 hypothetical prote
24	140.5	15.5	213	2	T51356 calcineurin B-like
25	138	15.3	193	2	I50676 gene Rem-1 protein
26	137	15.2	224	2	F96668 protein FLN19.5 (1
27	136	15.0	193	2	JH0816 neural vistin-11k
28	135	14.9	190	2	I51686 frequenin - Africa
29	135	14.9	193	2	S47565 calcium-binding pr

30	128	14.2	190	2	A55666 neurocalcin - frui
31	125	13.8	191	2	JH0815 neural vistin-11k
32	124	13.7	191	2	JH0616 neurocalcin (clone
33	122.5	13.6	155	2	S38877 tropoin C isoform
34	122.5	13.6	172	2	S38531 caltractin - mouse
35	121	13.4	190	2	S58303 related to neurom
36	121	13.4	190	2	S61168 hypothetical prote
37	121	13.4	270	2	JC7631 K+ channel-interac
38	119.5	13.2	212	2	I38424 hypothetical prote
39	119	13.2	214	2	T08922 hypothetical prote
40	118.5	13.1	254	2	T29566 hippocalcin - huma
41	118	13.1	193	2	UC2186 troponin C-1 - gla
42	117.5	13.0	158	2	A38397 calmodulin 8 (limp
43	117	12.9	151	2	A71409 troponin C isoform
44	116.5	12.9	155	2	S38878 diacylglycerol kin
45	116	12.8	791	2	A53691

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R:Barlow, K.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19442
A:Accession: T21563
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-311 <WILD>
A/Cross-references: EMBL:281072; PIDN:CAB03019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: clone F30A10
C/Genetics:
A:Gene: CESP:F30A10.1
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match 43.5%; Score 393; DB 2; Length 311;
Best Local Similarity 39.6%; Pred. No. 3.8e-21;
Matches 82; Conservative 52; Mismatches 47; Indels 26; Gaps 5;

QY 1 MGGSGSRLS-----KELLAEYDLTFTQELILAHRRCELLPOQRVSS 48
DB 111 MGNMSSLSELNLFSGGVFTREQLDEYDCTFTTKDILIRYKRYALNPKR--VPTN 167
QY 49 LRAQVP-----FEQILSPELKANPFKRICRVFSTSPAKDSLSPEDFLDLSVSDRA 102
DB 168 MGNMRAITTLTFEEVEKMKPELKENPFKRICEVES-EDGRNLSTDDLDLNFVSSEMA 226
QY 103 TPDIKSHVAFRTFXXXXXXXSRVLNVCULGEGEDTRLASSEMQLDINITEESDI 162
DB 227 PQLKLIKAFRIYDYDDELGHDDLKMIKIRSLTRD---ELSDVEVEFIRIIEEADL 282
QY 163 DRDGTINLSEFQHVISRSPDFASSPKI 189
DB 283 DDDSSINFAEFHVVSRSPDFIRTFHT 309

RESULT 2

T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R:McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ransperger, U.; Pohl, T.
Submitted to the EMBL Data Library, August 1999
A:Reference number: Z22005
A:Accession: T41632
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-174 <MCD>
A:Cross-references: EMBL:AL109850; PIDN:CAB52879.1; GSPDB:GN00068; SPDB:SPCC830.06
A:Experimental source: strain 972h-; cosmid c830
C:Genetics:
A:Gene: SPDB:SPCC830.06
A:Map position: 3
A:Introns: 18/1; 97/1; 134/3
A:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 21.7%; Score 196.5; DB 2; Length 174;
Best Local Similarity 24.4%; Pred. No. 4.5e-07;
Matches 44; Conservative 56; Mismatches 63; Indels 17; Gaps 4;

QY 1 MGGSGRLSKELLAEYQDLTFTKQELLARRFCCELLPQQRVTVESSLRQAQVPEQILS 60
DB 1 MQQSQIFEDLISN-----SFSNEIEIRKRTK-----IDANQSSIDRNEFLS 48

QY 61 LPELKANPFKERICRVFTSPAKSLSFEDFLDLVSFSDATPDIKSHYAFRIFXXXX 120
DB 49 IPSVASNPLASRLFSVDEDDGGD-VDFQEFINSLSVFSVHGNEEKLKFAFKIYDIDR 107

QY 121 XXXXXXXXSRVNLCTGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFQHVIRS 180
DB 108 GYISNGELYLVLMKMGV---TNLRDQLQIVDKTIMEVDKDRGKISFEFKDIVSGS 163

RESULT 3
JH0462
phosphoprotein phosphatase regulatory chain - yeast (Saccharomyces cerevisiae)
N:Alternate names: calcineurin chain B homolog; protein phosphatase 2B chain B; protein phosphatase 2B
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
C:Accession: JH0462; A45021; S33962; S38022; S38027; S34680; S52282
R:Kuno, T.; Tanaka, H.; Mukai, H.; Chang, C.D.; Hiraga, K.; Miyakawa, T.; Tanaka, C.
Biochem. Biophys. Res. Commun. 180, 1159-1165, 1991
A:Title: cDNA cloning of a calcineurin B homolog in Saccharomyces cerevisiae.
A:Reference number: JH0462; MUID:92062059; PMID:1659397
A:Accession: JH0462
A:Molecule type: mRNA
A:Residues: 1-175 <KUN>
A:Cross-references: EMBL:D10293; NID:g218409; PIDN:BAA01136.1; PID:g218410
R:Cyert, M.S.; Thorne, J.
Mol. Cell. Biol. 12, 3460-3469, 1992
A:Title: Regulatory subunit (CN1 gene product) of yeast Ca2+/calmodulin-dependent phosphatase
A:Reference number: A45021; MUID:92334345; PMID:1321337
A:Accession: A45021
A:Molecule type: DNA
A:Residues: 1-175 <CYE>
A:Cross-references: EMBL:M87508; NID:g171250; PIDN:AAA34505.1; PID:g171251
A:Note: sequence extracted from NCBI backbone (NCBIN:108731, NCBIIP:108732)
R:Cheret, G.; Mattheakis, L.C.; Sor, F.
Yeast 9, 661-667, 1993
A:Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cerevisiae
A:Reference number: S33960; MUID:93348778; PMID:8394042
A:Accession: S33962
A:Molecule type: DNA
A:Residues: 1-175 <CHE>
A:Cross-references: GB:X69765; NID:g296985; PIDN:CAA49421.1; PID:g296988
A:Experimental source: strain S288C
R:Wieman, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, J.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37825
A:Accession: S38022
A:Molecule type: DNA
A:Residues: 1-175 <WIE>
A:Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W
A:Experimental source: strain S288C
R:Maia e Silva, A.; Bossier, P.; Villela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; R
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38024
A:Accession: S38027

A:Molecule type: DNA
A:Residues: 1-175 <WAI>
A:Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W
A:Experimental source: strain S288C
R:Wieman, S.; Voss, H.; Schwager, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grot.
submitted to the EMBL Data Library, July 1993
A:Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome
A:Reference number: S34679
A:Accession: S34680
A:Molecule type: DNA
A:Residues: 31-175 <W12>
A:Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235
A:Experimental source: strain S288C
R:Pardo, J.M.
submitted to the EMBL Data Library, September 1993
A:Description: The protein phosphatase calcineurin is essential for NaCl tolerance in
A:Reference number: S52281
A:Accession: S52282
A:Molecule type: DNA
A:Residues: 1-175 <PAR>
A:Cross-references: EMBL:Z26521; NID:g473144; PIDN:CAA81290.1; PID:g473146
C:Genetics:
A:Gene: SGD:CNB1; YCN2
A:Cross-references: SGD:S0001673; MIPS:YKL190W
A:Map position: 11L
A:Introns: 18/1
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 1
F:2-175/Product: phosphoprotein phosphatase regulatory chain #status predicted <MAT>
F:21-52/Domain: calmodulin repeat homology <EF1>
F:53-85/Domain: calmodulin repeat homology <EF3>
F:90-122/Domain: calmodulin repeat homology <EF4>
F:131-163/Domain: calmodulin repeat homology <EF5>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experiment
Query Match 21.0%; Score 189.5; DB 2; Length 175;
Best Local Similarity 24.3%; Pred. No. 1.5e-06;
Matches 43; Conservative 54; Mismatches 63; Indels 17; Gaps 4;

QY 1 MGGSGRLSKELLAEYQDLTFTKQELLARRFCCELLPQQRVTVESSLRQAQVPEQILS 60
DB 1 MGAAPSKIYDGLLED---TNFDRDEIRLKRKFMKLDSSGSDIKN-----EFMS 48

QY 61 LPELKANPFKERICRVFTSPAKSLSFEDFLDLVSFSDATPDIKSHYAFRIFXXXX 120
DB 49 IPGVSSNPLAGIMEVDFDADNSGD-VDFQEFITGLSIFSGRSGKDEKLFARFIYDIDK 107

QY 121 XXXXXXXXSRVNLCTGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFQHVIR 177
DB 108 GFISNGELFVLKMGV---SNLDDQLQIVDRTIVENDSDGGRSLSEEFKNAI 160

RESULT 4
T47245
calcineurin regulatory chain [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C:Accession: T47245
R:Dieninger, M.; Tropisch, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z24421
A:Accession: T47245
A>Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 1-174 <DIE>
A:Cross-references: EMBL:Y12814; PIDN:CAA73345.1
A:Experimental source: strain 74 A
C:Genetics:
A:Gene: Can B
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 20.5%; Score 185.5; DB 2; Length 174;

Best Local Similarity 22.9%; Pred. No. 2.9e-06;
Matches 36; Conservative 52; Mismatches 56; Indels 13; Gaps 3;

QY 24 KQILLAHRFCELLPEQRTVSSRAOVPFOIISLPKLNPFKRCVSTSPAK 83
DB 20 REVDRLRRFEMLDKDNSTIER-----EEFLSLPQISTNPATRAIAFDENGCG 71

QY 84 DSLSFDFDLDSVSDFTATPDIKSHVAFRIYXXXXXXSRVNLCTGCEGDT 143
DB 72 D-VDFEFPVSGLSAFSRKKEKRLFAFVYIDRDGYSNGELFVLMKMGV----SN 126

QY 144 LSASEMKOLIDNLEESDIDRDGTINLSEFOHVISRS 180
DB 127 LKDOQLRIYDKTIMEDADLDCKISPEEFTKMENT 163

RESULT 5
A33391
Calcineurin regulatory chain - human
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
C:Accession: A33391
R:Quering, D.; Krinks, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A:Reference number: A33391; MUID:90126237; PMID:255868
A:Accession: A33391
A:Molecule type: mRNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705
C:Genetics:
A:Gene: GDB:PPPRL; CALNB
A:Cross-references: GDB:136804; OMIM:601302
A:Map position: 2p16-2p15
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:1-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asp) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status predicted

Query Match 19.0%; Score 171.5; DB 1; Length 170;
Best Local Similarity 27.0%; Pred. No. 3e-05;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFKRCVSTSPAKDSLSFDFDLDSVSDFTATPDIKSHVAFRI 115
DB 41 EEFMSLELOONPLVQRIYDIFDTD-GNGEYDFKEFIEGVSQFVKGDKEKLFARIRY 99

QY 116 XXXXXXXXXXSRVNLCTGCEGDTRLSASEMKOLIDNLEESDIDRDGTINLSEFOH 175
DB 100 DMKDQGISNGELFVLMKMGV----NNLKDQIQIYDKTIMADRDGGRISFEERCA 155

QY 176 VI 177
DB 156 VV 157

RESULT 6
S34127
Calcineurin regulatory chain (validated) - bovine
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C:Accession: I45831; J70297; S34127
R:Nargang, C.E.; Bottorff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A:Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A:Reference number: I45831; MUID:95102111; PMID:7803616
A:Accession: I45831
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <NA2>
A:Cross-references: EMBL:X17666; NID:g312968; PIDN:CAA5065.1; PID:g312969
R:Atken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A:Title: The structure of the B subunit of calcineurin.
A:Reference number: J70297; MUID:84132092; PMID:6321184
A:Accession: J70297
A:Molecule type: protein
A:Residues: 2-11, 'M', 13-153, 'S', 155-169 <AT>
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sitchak, M.D.; Thomson, J.A.; Fitzgibbon, submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66708; PDB:1JCO
A:Contents: annotation: X-ray crystallography, 2.5 angstroms, residues 2-170
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sitchak, M.D.; Thomson, J.A.; Fitzgibbon, Cell 82, 507-522, 1995
A:Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant cyclosporin A
A:Reference number: A56967; MUID:95360994; PMID:7543369
A:Contents: annotation: X-ray crystallography, 2.5 angstroms
C:Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F:1-170/Product: calcineurin regulatory chain #status experimental <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experiment
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experiment
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experiment
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status experiment
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status experiment

Query Match 19.0%; Score 171.5; DB 1; Length 170;
Best Local Similarity 27.0%; Pred. No. 3e-05;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFKRCVSTSPAKDSLSFDFDLDSVSDFTATPDIKSHVAFRI 115
DB 41 EEFMSLELOONPLVQRIYDIFDTD-GNGEYDFKEFIEGVSQFVKGDKEKLFARIRY 99

QY 116 XXXXXXXXXXSRVNLCTGCEGDTRLSASEMKOLIDNLEESDIDRDGTINLSEFOH 175
DB 100 DMKDQGISNGELFVLMKMGV----NNLKDQIQIYDKTIMADRDGGRISFEERCA 155

QY 176 VI 177
DB 156 VV 157

RESULT 7
J31220
Calcineurin regulatory chain, brain - mouse
N:Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: J31220
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A:Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase
A:Reference number: J31220; MUID:92392379; PMID:1325794
A:Molecule type: mRNA
A:Residues: 1-170 <VUK>
A:Cross-references: GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

A:Experimental source: brain
C:Comment: With calcineurin catalytic chain plays an important role in neural and nonneural
C:Genetics:
A:Gene: PP2B-beta-1
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipophilic
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 19.0%; Score 171.5; DB 1; Length 170;
Best Local Similarity 27.0%; Pred. No. 3e-05;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANFKERICRVFSTSPAKDSLSEDFDLVSVSDPATDIKSHYAFRIF 115
Db 41 EEPMSLPQLQNPVQRVIDFTD-GNGEVDFKEFIEGVSVKGDKEQKLRFAFRIF 99

QY 116 XXXXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILESDIDRDGTINLSEFQH 175
Db 100 DMDKDYIISNGELFQVLKMMVG-----NNLKDTQLQIVDKTIINADKDGGRISFEFCA 155

QY 176 VI 177
Db 156 VV 157

RESULT 8
S42716
calcineurin regulatory chain, long splice form - rat
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
N:Contains: calcineurin regulatory chain, short splice form
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S42716
R:Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
Biochim. Biophys. Acta 1217, 174-180, 1994
A:Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of calcineurin
A:Reference number: S42716; MUID:94153993; PMID:8110831
A:Accession: S42716
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-216 <CH2>
A:Cross-references: EMBL:D14425; NID:g286205; PIDN:BAA03318.1; PID:g286206
A:Accession: S42717
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'N', 48-216 <CH2>
A:Cross-references: EMBL:D14568; NID:g286255; PIDN:BAA03422.1; PID:g286256
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF hand
F:2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MAT>
F:48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MAT>
F:64-95/Domain: calmodulin repeat homology <EF1>
F:96-128/Domain: calmodulin repeat homology <EF2>
F:'N', 48-216/Product: calcineurin regulatory chain, short splice form precursor #status
F:133-165/Domain: calmodulin repeat homology <EF3>
F:174-206/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F:49/Modified site: aspartic acid (Asn) #status predicted

Query Match 19.0%; Score 171.5; DB 1; Length 216;
Best Local Similarity 27.0%; Pred. No. 4.2e-05;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANFKERICRVFSTSPAKDSLSEDFDLVSVSDPATDIKSHYAFRIF 115
Db 87 EEPMSLPQLQNPVQRVIDFTD-GNGEVDFKEFIEGVSVKGDKEQKLRFAFRIF 145

QY 116 XXXXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILESDIDRDGTINLSEFQH 175
Db 146 DMDKDYIISNGELFQVLKMMVG-----NNLKDTQLQIVDKTIINADKDGGRISFEFCA 201

QY 176 VI 177
Db 202 VV 203

RESULT 9
T22708
hypothetical protein F55C10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22708
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19603
A:Accession: T22708
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <WIL>
A:Cross-references: EMBL:Z74036; PIDN:CAA98489.1; GSPDB:GN00023; CESP:F55C10.1
A:Experimental source: clone F55C10
C:Genetics:
A:Gene: CESP:F55C10.1
A:Map position: 5
A:Introns: 159/2; 199/3; 213/1; 272/1; 312/3; 353/3

Query Match 18.8%; Score 169.5; DB 2; Length 369;
Best Local Similarity 25.0%; Pred. No. 0.00012;
Matches 45; Conservative 48; Mismatches 64; Indels 23; Gaps 6;

QY 3 GSGSRLSKELLAAYQ--DLTFTKQEIILAHRRFCELLPQEQRTVSSLRQVPEQIILS 60
Db 200 GADASLPMECSNFDAYELRLT-----RRFKL-----DVDGS--GSLSVVEEFS 243

QY 61 LPELKANPFKERICRVFSTSPAKDSLSEDFDLVSVSDPATDIKSHYAFRIFXXXX 120
Db 244 LPELQNPVQRVIDIFD-EDNGEVDFREFIQGISQFSVKGDKNKLFKFAFRIVMDRD 302

QY 121 XXXXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILESDIDRDGTINLSEFQHVSRS 180
Db 303 GFISNGELFQVLKMMVG-----NNLKDSQLQIVDKTILFHDKDGGKISFOEFCOWEHT 358

RESULT 10
T28047
hypothetical protein ZK856.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28047
R:Lloyd, C.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z20461
A:Accession: T28047
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <WIL>
A:Cross-references: EMBL:Z70783; PIDN:CAA94856.1; GSPDB:GN00023; CESP:ZK856.8
A:Experimental source: clone ZK856
C:Genetics:
A:Gene: CESP:ZK856.8
A:Map position: 5
A:Introns: 23/1; 42/1; 117/1

Query Match 18.3%; Score 165.5; DB 2; Length 195;
Best Local Similarity 22.3%; Pred. No. 0.0001;
Matches 44; Conservative 53; Mismatches 69; Indels 31; Gaps 6;

QY 1 MGSGLS-RLSKELLAAYQDLTFTKQEIILAHRRFCELLPQEQRTVSSLRQVPEQIIL 59

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Query Match      18.2% Score 164.5; DB 2; Length 213;
Best Local Similarity 22.1% Pred. No. 0.00013;
Matches 47; Conservative 53; Mismatches 68; Indels 45; Gaps 7;

QY 1 MGSGSGSRL-----SKELLAEOY-----DLTFLTKOEILLAHNRFCETLPOE 41
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MGNSSNSLISDAEMREIMDEFQCKVCVIAKQTFPPKNTISVKNHQLILTRYRFASL----- 56

QY 42 QRTVESSLRAGVAPPEQILSLPELKANPKPERICAFRTSPAKD-----SLSFEFDLL 95
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 -----DKMGQGLSKRDFINLPDLAVNPLGDDRIIDLFPLFGSDGDSKSGQLTFROFVITL 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 96 SVF-----SDTAPADIKS--HYAFRTFXKXXXXXXXXXXXXXSRVLNCLTGGEDPRLAS 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 AHFOPISKVKQNDALNSRKDLRFAPFKMYDLKNNVITYTEERKYLINSMVG-----ANITSD 168
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 148 EMKQIDINILTEESDIDRGGTINTLSEQFVIRS 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 QLDKIADKLTLEFADQDRGKISFEDFCRAMK 201
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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[illegible]

RESULT 14
A44307
calcineurin regulatory chain 1 - fruit fly (Drosophila melanogaster)
N:Alternate names: calcineurin beta subunit; calcineurin chain B-1; phosphoprotein phosph
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A44307
R:Guerin, D.; Montell, C.; Klee, C.B.
J. Biol. Chem. 267, 22542-22549, 1992
A:Title: Molecular cloning and characterization of the genes encoding the two subunits o
A:Reference number: A44307; MUID:93054551; PMID:1331060
A:Accession: A44307
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
A:Note: sequence extracted from NCBI backbone (NCBIP:117113)
C:Genetics:
A:Gene: FlyBase:CanB
A:Cross-references: FlyBase:FBgn0010014
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.4%; Score 157.5; DB 2; Length 170;
Best Local Similarity 23.2%; Pred. No. 0.00032;
Matches 36; Conservative 47; Mismatches 59; Indels 13; Gaps 3;

Qy 26 BILLAHRFCCELLPQEQTVESLRAQVPPQILSLPAKDS 85
Db 19 EIRLGKRF-----RKLDNSGALSIDFMSLPQLQONPLVQRVIDFD-ADNGE 69

Qy 86 LSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXXSRVLCNLTGEGEDTFLS 145
Db 70 VDFKEFIQGVQSVRGSKLRFAPRIYDMNDGVISNGELFQVLKMMVG-----NNLK 125

Qy 146 ASEMQLIDNLESDDRDCTINLSEFQHVSR 180
Db 126 DTQLQIVDKTICFADKDEDKISDFECFSYVGN 160

RESULT 15
T51357
calcineurin B-like protein 2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Dec-2000
C:Accession: T51357
R:Kudla, J.; Xu, Q.; Harter, K.; Gruissem, W.; Luan, S.
Proc. Natl. Acad. Sci. U.S.A. 96, 4718-4723, 1999
A:Title: Genes for calcineurin B-like proteins in Arabidopsis are differentially regulat
A:Reference number: 224109; MUID:99218346; PMID:10200328
A:Accession: T51357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <KUD>
A:Cross-references: EMBL:AF076252; PIDN:AAC26009.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: CBL2
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 17.3%; Score 156.5; DB 2; Length 226;
Best Local Similarity 25.0%; Pred. No. 0.00056;
Matches 47; Conservative 46; Mismatches 84; Indels 11; Gaps 6;

Qy 2 GSGSRLSKELLAQVODLTETLTKOELLAHRRFCCELLPQEQTVESLRAQVPPQILSL 61
Db 28 GGLG---DPELLA--RDTVF--SVSEIEALYELFKI---SSAVIDDGLINKKEEFQALFK 78
Qy 62 PELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXX 121
Db 79 TNKESLFADRVDFDLDTK-HNGILGFEEFARALSVFHPNAPIDDKIHFSQLYDLKQOG 137
Qy 122 XXXXXXSRVLCNLTGEGEDTFLSASEMKQLIDNLESDDRDCTINLSEFQHVSR 181
Db 138 FIERQEVKQMVVATLAE-SGMNLKDTVIDIIDKTFEEDTKHDKGIDKEWRSVLVRHP 196
Qy 182 DFASSEFKI 189
Db 197 SLLKNMTL 204

Search completed: January 17, 2003, 12:52:18
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:49:14 ; Search time 13 Seconds
(without alignments)
609.383 Million cell updates/sec

Title: US-09-878-454a-2x
Sequence: 1 MGSGSRSLSKELLAEYQDLT.....EFQHVISRSPDPASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt-40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	904	100.0	191	1	KIP1_HUMAN
2	856	94.7	191	1	KIP1_MOUSE
3	855	94.6	191	1	KIP1_MOUSE
4	326	36.1	187	1	KIP2_MOUSE
5	324	35.8	187	1	KIP2_MOUSE
6	201.5	22.3	177	1	CALB_MOUSE
7	196.5	21.7	174	1	CALB_MOUSE
8	185.5	20.5	174	1	CALB_MOUSE
9	184.5	20.4	174	1	CALB_MOUSE
10	171.5	19.0	169	1	CALB_MOUSE
11	171.5	19.0	169	1	CALB_MOUSE
12	161.5	17.9	170	1	CALB_MOUSE
13	160	17.7	194	1	CALB_MOUSE
14	157.5	17.4	190	1	CALB_MOUSE
15	156	17.3	194	1	CALB_MOUSE
16	155.5	17.2	178	1	CALC_MOUSE
17	153.5	17.0	175	1	CALC_MOUSE
18	148.5	16.4	189	1	NCB2_MOUSE
19	146.5	16.2	186	1	NCB2_MOUSE
20	144	14.8	214	1	TESE_MOUSE
21	133	14.7	190	1	TESE_MOUSE
22	133	14.7	190	1	TESE_MOUSE
23	132.5	14.7	195	1	TESE_MOUSE
24	131	14.5	192	1	TESE_MOUSE
25	131	14.5	214	1	TESE_MOUSE
26	130	14.4	189	1	NCB1_MOUSE
27	130	14.4	189	1	NCB1_MOUSE
28	130	14.4	190	1	NCB1_MOUSE
29	126	13.9	190	1	NCB1_MOUSE
30	125	13.8	192	1	NCB1_MOUSE
31	123	13.6	189	1	NCB1_MOUSE
32	122.5	13.6	155	1	TPC2_MOUSE
33	122.5	13.6	172	1	CATR_MOUSE

34	120	13.3	190	1	VTS2_RAT
35	119.5	13.2	172	1	CATR_HUMAN
36	119	13.2	192	1	NCAD_MOUSE
37	119	13.2	192	1	NCAD_MOUSE
38	118.5	13.1	155	1	TPC3_MOUSE
39	117.5	13.0	158	1	TPC3_MOUSE
40	117	12.9	804	1	KDGB_HUMAN
41	116	12.8	189	1	NCB1_MOUSE
42	116	12.8	189	1	NCB1_MOUSE
43	116	12.8	791	1	KDGB_HUMAN
44	115	12.7	192	1	KDGB_HUMAN
45	113.5	12.6	801	1	KDGB_RAT

ALIGNMENTS

RESULT 1

KIP1_HUMAN STANDARD: PRT; 191 AA.
AC Q99828: 000735; 000693; Q99971; Q9654;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs interacting protein) (Kinase interacting protein) (KIP) (SNK)
DE Interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98040126; PubMed=9372844;
RT Wu X., Lieber M.R.;
RL "Interaction between DNA-dependent protein kinase and a novel protein, KIP.";
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Petal liver;
RT MEDLINE=97184102; PubMed=9030514;
RL Naik U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts with the integrin alpha1b cytoplasmic domain.";
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=20284952; PubMed=10826701;
RT Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RL "Genomic structure of mouse and human genes for DNA-PKcs interacting protein (KIP).";
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE=Cervix;
RT Strassberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RP STRUCTURE BY NMR OF 9-191.
RX MEDLINE=20283154; PubMed=10822252;
RA Huang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and the alpha1b-integrin cytoplasmic domain suggest a mechanism for RT calcium-regulated recognition: homology modelling and NMR studies.";
J Mol. Recognit. 13:83-92(2000).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

DR SMART: SM00054; EFH: 2.
 DR PROSITE; PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21763 MW; C85B03A19F9D9AC CRC64;

Query Match 94.7%; Score 856; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 7.7e-58;
 Matches 168; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELAEYODLFTLKQELLHRRFCELLPOEORTVSSLAQVFEQILS 60
 DB 1 MGSGSRLSKELAEYODLFTLKQELLHRRFCELLPOEORTVSSLAQVFEQILS 60
 QY 61 LPELKANPFEKRICRVSTSPKNDLSFEEDFLDLVSFSDTAPDISHYAFRIFFXXXX 120
 DB 61 LPELKANPFEKRICRVSTSPKNDLSFEEDFLDLVSFSDTAPDISHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVNCLTGEGEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLDRELSQLVNCLTGEEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

RA Scaffidi J., Staib U., Betschler-Hahn J., Streibhardt K., Kuhl D.,
 "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 integrin-binding protein and are regulated dynamically with synaptic
 plasticity.";
 EMBO J. 18:5528-5539(1999).
 RN 11)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 integrin-binding protein and are regulated dynamically with synaptic
 plasticity.";
 EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING OF THE INTEGRIN
 CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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 or send an email to license@sib-sib.ch).

DR EMBL: AF136585; AAF08368.1;
 DR HSSP: Q99828; IDGV.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 DR ProDom: PD000012; EF-hand; 1.

DR SMART: SM00054; EFH: 2.
 DR PROSITE; PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21800 MW; 3B0B0228879FC7 CRC64;

Query Match 94.6%; Score 855; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 9.2e-58;
 Matches 168; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELAEYODLFTLKQELLHRRFCELLPOEORTVSSLAQVFEQILS 60
 DB 1 MGSGSRLSKELAEYODLFTLKQELLHRRFCELLPOEORTVSSLAQVFEQILS 60
 QY 61 LPELKANPFEKRICRVSTSPKNDLSFEEDFLDLVSFSDTAPDISHYAFRIFFXXXX 120
 DB 61 LPELKANPFEKRICRVSTSPKNDLSFEEDFLDLVSFSDTAPDISHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVNCLTGEGEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLDRELSQLVNCLTGEEDTRLASSEMQLDNIIEESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RA Saito T.;
 "Structure, expression profile and chromosomal location of an isolog
 of DNA-PKcs interacting protein (KIP) gene.";
 Biochim. Biophys. Acta 1444:143-147(1999).
 RN 11)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99132027; PubMed-9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Horii T.,
 "Structure, expression profile and chromosomal location of an isolog
 of DNA-PKcs interacting protein (KIP) gene.";
 Biochim. Biophys. Acta 1444:143-147(1999).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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 or send an email to license@sib-sib.ch).

DR EMBL: AB01080; BAA36545.1;
 DR HSSP: Q99828; IDGV.
 DR MG: 1929293; KIP2.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 3.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFH: 2.
 DR PROSITE; PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBDB0B6F5C CRC64;

Query Match 36.1%; Score 326; DB 1; Length 187;
Best Local Similarity 34.7%; Pred. No. 1.2e-17;
Matches 67; Conservative 53; Mismatches 61; Indels 12; Gaps 4;

QY 1 MGGSGRLSKELLAAYQDLTFLTKQETLLAHRFFCE-----LLPQORTVSSSLRAQVPFE 56
DB 1 MGNKQITITEEQLDNYQCTFFNKKDILKLSHRYELAPNLVPMYR---KSPIVHVPM 57
QY 57 QILSPELKANPFRKICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116
DB 58 LIOMPELRENPFRKIVAEFS-EDGEGLTFNDFVMSVLCESAPRELKANYAFKIYD 116
QY 117 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQIDNILEESIDRGTINLSEFOHV 176
DB 117 FNTDNFKEDLEMTLARTL-----KSELEDEVLVCDKVEEADLDGGLGFADFEDM 172
QY 177 ISRSPDFASSFKI 189
DB 173 IAKAPDFLSTFHI 185

RESULT 5
KIP2_HUMAN
ID KIP2_HUMAN STANDARD; PRT; 187 AA.
AC 075838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Kinase interacting protein 2 (KIP 2).
GN KIP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Fetal brain;
RX MEDLINE=99132027; PubMed=9931475;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
RT "Structure, expression profile and chromosomal location of an isolog
of DNA-PKcs interacting protein (KIP) gene.";
RL Biochim Biophys Acta 1444:143-147(1999).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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or send an email to license@isb-sib.ch).
CC EMBL; AB012955; BAA33584.1;
CC HSP; Q99828; 1DGV.
CC MIM; 605564;
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00036; ehand; 3.
CC ProDom: PD000012; EF-hand; 1.
CC SMART: SM00054; EFh; 2.
CC PROSITE: PS00018; EFHAND; 2.
CC Calcium-binding; Repeat.
KW CA_BIND 116 EF-HAND 1 (POTENTIAL).
FT CA_BIND 127 EF-HAND 2 (POTENTIAL).
FT CA_BIND 157 168
SQ SEQUENCE 187 AA; 21643 MW; D51P6C25AD381BEF CRC64;

Query Match 35.8%; Score 324; DB 1; Length 187;
Best Local Similarity 34.7%; Pred. No. 1.7e-17;
Matches 67; Conservative 53; Mismatches 61; Indels 12; Gaps 4;

QY 1 MGGSGRLSKELLAAYQDLTFLTKQETLLAHRFFCE-----LLPQORTVSSSLRAQVPFE 56
DB 1 MGNKQITITEEQLDNYQCTFFNKKDILKLSHRYELAPNLVPMYR---KSPIVHVPM 57
QY 57 QILSPELKANPFRKICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116
DB 58 LIOMPELRENPFRKIVAEFS-EDGEGLTFNDFVMSVLCESAPRELKANYAFKIYD 116
QY 117 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQIDNILEESIDRGTINLSEFOHV 176
DB 117 FNTDNFKEDLEMTLARTL-----KSELEDEVLVCDKVEEADLDGGLGFADFEDM 172
QY 177 ISRSPDFASSFKI 189
DB 173 IAKAPDFLSTFHI 185

Db 1 MGNKQITITEEQLDNYQCTFFNKKDILKLSHRYELAPNLVPMYR---KSPIVHVPM 57
QY 57 QILSPELKANPFRKICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116
DB 58 LIOMPELRENPFRKIVAEFS-EDGEGLTFNDFVMSVLCESAPRELKANYAFKIYD 116
QY 117 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQIDNILEESIDRGTINLSEFOHV 176
DB 117 FNTDNFKEDLEMTLARTL-----KSELEDEVLVCDKVEEADLDGGLGFADFEDM 172
QY 177 ISRSPDFASSFKI 189
DB 173 IAKAPDFLSTFHI 185

RESULT 6
CALB_NAEGR
ID CALB_NAEGR STANDARD; PRT; 177 AA.
AC P42322;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB1
OS Naegleria gruberi.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
OX NCBI_TaxID=5762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEG;
RX MEDLINE=9517399; PubMed=7867946;
RA Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;
RT "A calcineurin-B-encoding gene expressed during differentiation of
the amoeboid flagellate Naegleria gruberi contains two introns.";
RL Gene 154:39-45(1995).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
SENSITIVITY (BY SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
SUBUNIT (B) (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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or send an email to license@isb-sib.ch).
CC EMBL; U04380; AAA81896.1;
CC HSP; P06705; LAUI.
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00036; ehand; 4.
CC ProDom: PD000012; EF-hand; 2.
CC SMART: SM00054; EFh; 4.
CC PROSITE: PS00018; EFHAND; 4.
CC Calcium-binding; Repeat.
KW CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).
FT CA_BIND 70 81 EF-HAND 2 (BY SIMILARITY).
FT CA_BIND 107 118 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 177 AA; 20057 MW; 01D4A48E6947E97C CRC64;

Query Match 22.3%; Score 201.5; DB 1; Length 177;
Best Local Similarity 26.4%; Pred. No. 3.1e-08;
Matches 47; Conservative 50; Mismatches 68; Indels 13; Gaps 3;

QY 1 MGGSGRLSKELLAAYQDLTFLTKQETLLAHRFFCE-----LLPQORTVSSSLRAQVPFE 56
DB 1 MGNKQITITEEQLDNYQCTFFNKKDILKLSHRYELAPNLVPMYR---KSPIVHVPM 57
QY 57 QILSPELKANPFRKICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116
DB 58 LIOMPELRENPFRKIVAEFS-EDGEGLTFNDFVMSVLCESAPRELKANYAFKIYD 116
QY 117 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQIDNILEESIDRGTINLSEFOHV 176
DB 117 FNTDNFKEDLEMTLARTL-----KSELEDEVLVCDKVEEADLDGGLGFADFEDM 172
QY 177 ISRSPDFASSFKI 189
DB 173 IAKAPDFLSTFHI 185

DB 1 MGTTSSIRPEVEEMOKGNFTOKELKKYRKKLDKNGTISK-----DEFIM 52

QY 61 LPELKNPFRERICRVSTSPAKDSLSEFEDLLSVSPDAPDKSHVAFRIEXXXXX 120

DB 53 IPELAVNPLVKRIVSIFDEN-GDGSVNFKEITALSVFNAGDQKRIEFKRYDIDGD 111

QY 121 XXXXXXXXSLVNCNLTEGEDTRLSASEMQLDNIIEESDIDRGITINSEFOHVIS 178

DB 112 GYISNGELFTVLMKMGV-----NNLSVDLOQIDVKTILEDEDDGKISFEFPKRTLS 165

RESULT 7

CALB_SCHPO STANDARD; PRT; 174 AA.

AC 09U093;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)

DE (Calcineurin regulatory subunit).

GN CNB1 OR SPCC830.06.

OS Schizosaccharomyces pombe (fission yeast)

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972.

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,

RA Gentles S., Godle A., Hamlin N., Harris D., Hidalgo J., Hodgson A.,

RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Stammers M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Koestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleure V., Mottier S.,

RA Gilbert M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Lucas M., Rochez M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;

RA "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,

CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM

CC SENSITIVITY (BY SIMILARITY).

CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY

CC SUBUNIT (B) (BY SIMILARITY).

CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING

CC SITES (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

CC

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CC or send an email to license@sib-sib.ch).

DR EMBL: AL109850; CAB52879.1; -

DR HSSP: P06705; IAU1.

DR InterPro: IPR002048; EF-hand.

DR InterPro: IPR001125; Recoverin.

DR Pfam: PF00036; ehand; 4.

DR PRINTS: PR00450; RECOVERIN.

DR ProDom: PD000012; EF-hand; 1.

DR SMART: SM00054; Efh; 4.

DR PROSITE: PS00018; EF_HAND; 4.

KW Calcium-binding; myristate.

FT CA_BIND 34 45

FT CA_BIND 66 77

FT CA_BIND 103 114

FT CA_BIND 144 155

FT SEQUENCE 174 AA; 19675 MW; EEF38FE74959442E CRC64;

Query Match 21.7%; Score 196.5; DB 1; Length 174;

Best Local Similarity 24.4%; Pred. No. 7.2e-08;

Matches 44; Conservative 56; Mismatches 63; Indels 17; Gaps 4;

QY 1 MGSGSRLSKELLAEDYDITFLTKOELLARHRCCELLPQDQRTVESSLRAQVFEQILS 60

DB 1 MGQSQSIQFEDLISN-----SFSMELEIRIKRKRIK-----IDANQSGSIDRNEFLS 48

QY 61 LPELKNPFRERICRVSTSPAKDSLSEFEDLLSVSPDAPDKSHVAFRIEXXXXX 120

DB 49 IPSVANSPLASRLFSVDEDEGGCD-VDFQEFINSLSVSVGNKNEELKRAFIYDIDRD 107

QY 121 XXXXXXXXSLVNCNLTEGEDTRLSASEMQLDNIIEESDIDRGITINSEFOHVIS 180

DB 108 GYISNGELFTVLMKMGV-----TNLRDQLOQIDVKTILEYDKDRDKISFEFPKRTLS 163

RESULT 8

CALB_NEUCR STANDARD; PRT; 174 AA.

AC P87072; O13408;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)

DE (Calcineurin regulatory subunit).

GN CNB-1 OR CNB-B.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=74A;

RX MEDLINE=98007857; PubMed=9349701;

RA Prokisch H., Yarden O., Dieminger M., Tropeschug M., Barthelmeß I.B.;

RA "Impairment of calcineurin function in Neurospora crassa reveals its

RA essential role in hyphal growth, morphology and maintenance of the

RA apical Ca²⁺ gradient.";

RL Mol. Gen. Genet. 256:104-114(1997).

CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,

CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM

CC SENSITIVITY.

CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY

CC SUBUNIT (B).

CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING

CC SITES.

CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

CC

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DB 1 CAASKYIDGLED-----TNFDRDEIERLRKRFMKLDRSSGSDKN-----EFMSI 48

QY 62 PELANPKFERICVFSTSPAKDSLSFEDFLDLSFSDTAPODKSHYAFREXXXXX 121

DB 49 PGVSNPLAGIMEVFDNDSGD-VDRQEFITGLSIFSGRSKDKLRFARFYDIDKG 107

QY 122 XXXXXXSRVNCITGEGEDRLSASEMKQIDNILESDIDRGTINLSEFOHYI 177

DB 108 FISNGELFVLKIMVG-----SNLDEQLQOIVDTIVENDSDGGRSLSEFEKKNI 159

RESULT 10

CALE_HUMAN STANDARD; PRT; 169 AA.

AC P06705; P15117; Q08044;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calciineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).

GN PPP3R1 OR CNB OR CNA2.

OS Homo sapiens (human),

OS Bos taurus (Bovine), and

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606, 9913, 10116;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES-Human;

RA MEDLINE=90126237; PubMed=2558868;

RA Guerini D., Krinks M.H., Silela J.M., Hahn W.E., Klee C.B.;

RT "Isolation and sequence of a cDNA clone for human calciineurin B, the

RT Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein

RT phosphatase.";

RL DNA 8:675-682(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES-Bovine;

RA Nargang C.E., Bottorff D.A., Adachi K.;

RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-168.

RC SPECIES-Bovine; TISSUE-Brain;

RA MEDLINE=84132092; PubMed=6321184;

RA Aitken A., Klee C.B., Cohen P.;

RT "The structure of the B subunit of calciineurin.";

RL Eur. J. Biochem. 139:663-671(1984).

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES-Rat;

RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;

RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC SPECIES-Rat; TISSUE-Brain, and Testis;

RA MEDLINE=94153993; PubMed=8110831;

RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;

RT "cDNA cloning of an alternatively spliced isoform of the regulatory

RT subunit of Ca2+/calmodulin-dependent protein phosphatase (calciineurin

RT B alpha 2).";

RL Biochim. Biophys. Acta 121:174-180(1994).

RN [6]

RP CALCULUM-BINDING DATA.

RC SPECIES-Bovine;

RA MEDLINE=80101597; PubMed=293720;

RA Klee C.B., Crouch T.H., Krinks M.H.;

RT "Calciineurin: a calcium- and calmodulin-binding protein of the

RT nervous system.";

RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RC SPECIES-Bovine;

RA MEDLINE=95360994; PubMed=7543369;

RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.;

RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;

RT "X-ray structure of calciineurin inhibited by the immunophilin-

RT Immunosuppressant FKBP12-FK506 complex.";

RL Cell 82:507-522(1995).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RC SPECIES-Human;

RA MEDLINE=96097077; PubMed=8524402;

RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.;

RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.;

RA Gashtiel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.;

RT "Crystal structures of human calciineurin and the human FKBP12-FK506-

RT calciineurin complex.";

RL Nature 378:641-644(1995).

CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,

CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE, CONFERS CALCIUM

CC SENSITIVITY.

CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY

CC SUBUNIT (B).

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE

CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.

CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.

CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING

CC SITES.

CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

CC

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CC -----

DR EMBL: M30773; AAB08721.1; -

DR EMBL: X71666; CAA50659.1; -

DR EMBL: L03554; AAA40854.1; -

DR EMBL: D14458; BAA03422.1; -

DR EMBL: D14425; BAA03318.1; -

DR PIR: A33991; A33391.

DR PIR: S34127; S34127.

DR PIR: J70297; J70297.

DR PIR: S42716; S42716.

DR PIR: S42717; S42717.

DR PDB: 1A01; 03-DEC-97.

DR PDB: 1TCO; 12-FEB-97.

DR Genew; HGNC:9317; PPP3R1.

DR InterPro: IPR0020A8; EF-hand.

DR Pfam: PF00036; EF-hand.

DR ProDom; PD000012; EF-hand; 4.

DR SMART; SM00054; EFh; 4.

DR PROSITE; PS00018; EF_HAND; 4.

KW Calcium-binding; Repeat; Alternative splicing; Myristate;

KW 3D-structure.

FT INIT_MER 0

FT LIPID 1

FT CA_BIND 30

FT CA_BIND 62

FT CA_BIND 99

FT CA_BIND 140

FT VARSPIC 1

FT MYRISTATE.

FT EF-HAND 1.

FT EF-HAND 2.

FT EF-HAND 3.

FT EF-HAND 4.

G -> MEDTDLQSOIFPPTEKNEKKKDKHFRQKYPFSR

ELYNLIFDRKG (IN ISOFORM 2).

C -> M (IN REF. 3).

C -> S (IN REF. 3).

SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 19.0%; Score 171.5; DB 1; Length 169;

Best Local Similarity 27.0%; Pred. No. 5.4e-06;

```

Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2
QY 56 EQILSPELKPANPKERICRVFTSPAKDSLSPEDFLDLLSVFSDTATPDIKSHYAFRI 115
Db 40 EEFMSLPELQNVLRVQVDFDFTD-GNGEVDFKEFIEGVQSFVKGDKEQKLREAFRIY 98
QY 116 XXXXXXXXXXXXSLVNLCLTGEGEDTRLSEASEMKQLIDNILEESDIDRDGINLSEFQH 175
Db 99 DNDKDGYSINGELFQVLKMMVVG-----NNLKDTQLQIVDKTIINADKDGGRISFEFCA 154
QY 176 VI 177
Db 155 VV 156

RESULT 11
CALB_MOUSE
ID CALB_MOUSE STANDARD; PRT; 169 AA.
AC Q63810.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE 1).
GN PFP3R1 OR CNB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92392379; PubMed=1325794;
RT Ueki K., Muramatsu T., Kincaid R.L.;
RT "Structure and expression of two isoforms of the murine calmodulin-
RT dependent protein phosphatase regulatory subunit (calcineurin B).";
RT Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIM, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S43864; AAB23171.1; .
CC R5SP; P06705; IAU1.
CC DR DR
CC MGD; MGI:107172; Pp3r1.
CC DR DR
CC InterPro; IPR002048; EF-hand.
CC DR DR
CC Pfam; PF00036; ehand; 4.
CC DR DR
CC ProDom; PD000012; EF-hand; 2.
CC DR DR
CC SMART; SM00054; EFh; 4.
CC DR DR
CC PROSITE; PS00018; EF_HAND; 4.
CC DR DR
CC Calcium-binding; Repeat; Myristate.
CC KW
CC INIT_MET 0 0 BY SIMILARITY.
CC FT FT
CC FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
CC FT FT
CC FT CA_BIND 30 41 EF-HAND 1.
CC FT FT
CC FT CA_BIND 62 73 EF-HAND 2.
CC FT FT
CC FT CA_BIND 99 110 EF-HAND 3.
CC FT FT
CC FT CA_BIND 140 151 EF-HAND 4.
CC FT FT
CC SQ SEQUENCE 169 AA; 19142 MW; D1490BASB2F432F CRC64;

```

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Massaman D.A., Weinstein A., Welschbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zheng L.,
Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL: U56245; AAC47350.1; -
CC EMBL: AE003840; AAF59195.1; ALT_SEQ.
CC HSSP: P06705; ITCO.
CC DR EMBL: F890015614; CanB2
CC DR EMBL: F890015614; CanB2
CC DR InterPro: IPR002048; EF-hand.
CC DR InterPro: IPR001125; Recoverin.
CC DR Pfam: PF00036; ehand; 4.
CC DR PRINTS: PR00450; RECOVERIN.
CC DR ProDom: PD000012; EF-hand; 2.
CC DR SMART: SM00054; EFh; 4.
CC DR PROSITE: PS00018; EF_HAND; 4.
CC KW Calcium-binding; Repeat.
CC FT CA-BIND 31 42 EF-HAND 1 (POTENTIAL).
CC FT CA-BIND 63 74 EF-HAND 2 (POTENTIAL).
CC FT CA-BIND 100 111 EF-HAND 3 (POTENTIAL).
CC FT CA-BIND 141 152 EF-HAND 4 (POTENTIAL).
CC SO SEQUENCE. 170 AA; 19267 MW; FDB1BD9D85A4BDEC CRC64;

Query Match 17.9%; Score 161.5; DB 1; Length 170;
Best Local Similarity 21.9%; Pred. No. 3; 1e-05;
Matches 39; Conservative 52; Mismatches 68; Indels 19; Gaps 4;

OY 3 GGGSRSLKRLAEYQDITLTQKQELLARREPELLPOGRYVESLRQVPEQLISLP 62
DB 2 GNETSLPMKCNFD-----ADEIRRLGRF-----RKDLNNGALSDVERMSLP 47
OY 63 ELKANPFERICRVSTSPAKDLSPEFDLISVSDPATPDIKSHVAFRIKXXXXXX 122
DB 48 ELQONPIVQGVDFID-AGNGNEVDFKEITQGVSGSVGDKSLRFARITDMNDG 106
OY 123 XXXXXXSLVNCITGEGEDFRLSASEMQLDNIIEESDIDRGTINLSEFQHVIS 180
DB 107 ISNGELFVLMKMGV---NNLKDTQLOQIVDKTIGFADKDEGKISPFECVQNT 160

RESULT 13
CA22_MOUSE STANDARD: PRT; 194 AA.
AC 062877;
DT 01-NOV-1997 (Rel. 35, Last created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (Std470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat: TISSUE-Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd K.K., Dewitt N.D., Chang A., Mills K.,
RA Stul E.S.;
RT "A novel Ca²⁺-binding protein, p22, is required for constitutive
RT membrane traffic.";
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat: TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
RA Takemoto K., Ohtsuka C., Murekami H., Nakamura N., Kanazawa H.;
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na⁺/H⁺
RT exchanger.";
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBD databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN-C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Koehne H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch R.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -1- PTM: BOTH N-MYRISTYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
CC EMBL: U39875; AAB04146.1; -
CC EMBL: AB070350; BAB63369.1; -
CC EMBL: AB025217; BAA64688.1; -

DR EMBL; AK005067; BAB23791.1; -
DR HSSP; P06705; LAUI.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF-HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT MET 0 0
FT LIPID 1 1 MYRISTATE (PROBABLE).
FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
FT MUTAGEN 133 133 *E->A: LOSS OF TARGETING/FUSION FUNCTION.
SQ SEQUENCE 194 AA; 22301 MW; E2DF35E5F627B8231 CRC64;
Query Match 17.7%; Score 160; DB 1; Length 194;
Best Local Similarity 24.2%; Pred. No. 5e-05;
Matches 47; Conservative 44; Mismatches 71; Indels 32; Gaps 6;
QY 5 GSR-----LSKELLAEVDLTFTKOBILLAHRRFCCELLPQEQRTVESSLRAQVPEQILS 60
DB 1 GSRATLLRDEELEEIKETGFSHSOITRLYSRFTSLDKGENTLSR-----EDFOR 52
QY 61 LPCLKANPKERICRVFSTSPARKSLSFEDFLDLISVF-----SDTATPD----- 105
DB 53 IPELAINPLGDRINAF-FSEGEDQVNFGRFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111
QY 106 IKSHYAFRFXKXXXXXXXSRVNLCTGEGEDTRLSASEMQLDNIILEESDIDRD 165
DB 112 NKLHFAFLYLDKDKISRDELQVLRMMVG-----VNISDEQLGSIADRTIQEQDQGD 167
QY 166 GTINLSEFOHVSIR 179
DB 168 SAISFTFVKVLEK 181
RESULT 14
CALB.DROME STANDARD; PRT; 170 AA.
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin."
RL J. Biol. Chem. 267:22542-22549 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinartz K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
FT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
CC -!- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B). THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC
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CC
CC EMBL; M97215; AAA28411.1; -
CC EMBL; AE003434; AAF46026.1; -
CC HSSP; P06705; ITCO.
CC FlyBase; FBgn0010014; CanB.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF-HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19341 MW; 77D89BE9BD961900 CRC64;
Query Match 17.4%; Score 157.5; DB 1; Length 170;
Best Local Similarity 23.2%; Pred. No. 6.3e-05;
Matches 36; Conservative 47; Mismatches 59; Indels 13; Gaps 3;
QY 26 EILLAHRRFCCELLPQEQRTVESSLRAQVPEQILSLPELKNPKFKERICRVFSTSPAKDS 85
DB 19 EIRRLGRF-----RKLDLNSGALSIDFMSLPELQONPLVORVIDFD-ADNGNE 69

QY 86 LSEFDLLSVSDTATPDIKSHYAFRIFXXXXXXXXXXSRVNCLTGEGEDRPLS 145
 DB 70 VDFEFIOGVSOFSRGDKLSKLFARIFRDMNDGYSINSELOVKLMVG-----NNLK 125
 QY 146 ASEMKOLINDILEESDIDRGCTINLSEFOHVISRS 180
 DB 126 DTQLQOIVDKTICFADKDEDKISFDEFCSVGNT 160

RESULT 15

CA22_HUMAN STANDARD: PRT; 194 AA.
 AC Q99653;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog).
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA MEDLINE=97057295; PubMed=8901634;
 RA Lin X., Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strusberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTRAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; U61538; AAB37770.1; -
 DR EMBL; BC001646; AAH01646.1; -
 DR HSSP; P06705; IAU1.
 DR MIM; 606968; -
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 KW Calcium-binding; Repeat; Myristate; Phosphorylation.
 FT INIT_MET 0
 FT LIPID 1
 FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DEE5F03C88380 CRC64;
 Query Match 17.38; Score 156; DB 1; Length 194;
 Best Local Similarity 23.78; Pred. No. 0.0001;
 Matches 46; Conservative 44; Mismatches 72; Indels 32; Gaps 6;
 QY 5 GSR-----LSKELLAEDYDLFELTQKOEILLARFCELLPQORTVSSLSRAQVEFOILS 60
 DB 1 GSRASITLRLDBELEIEIKKEIGFSHSQITRLYSRTSLDKENGTLNR-----EDFOR 52
 QY 61 LPELKAPFERICRVRVSTSPAKDSLSFEDFLDLVSF-----SDATPD----- 105
 DB 53 IPELAINPLDGRILINAFPE-GEQVNFQGMRTLAHFRPLEDNEKSKDVNGPEPLNSRS 111
 QY 106 IKSHYAFRIFXXXXXXXXXXSRVNCLTGEGEDRPLSASEMKOLINDILEESDIDRD 165
 DB 112 NKLHFAFRLYDLDDKDISDELQVLRMVG-----VNISDEOLGSIADRTIQEADQGD 167
 QY 166 GTINLSEFOHVISR 179
 DB 168 SAISFTEFVKLEK 181

Search completed: January 17, 2003, 12:51:16
 Job time: 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:49:40 ; Search time 31 Seconds
(without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454a-2x

Sequence: 1 MGGSGSRSLKELLAEYQDLT.....EFOHVISRSPDFASFEKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	43.5	311	5	Q93640
2	344	38.1	185	11	Q96077
3	337	37.3	187	4	Q96077
4	320.5	35.5	206	5	Q96077
5	219	24.2	54	6	Q96077
6	214.5	23.7	180	5	Q96077
7	186	20.6	175	10	Q96077
8	186	20.6	175	10	Q96077
9	184	20.4	175	10	Q96077
10	169.5	18.8	169	5	Q96077
11	169.5	18.8	244	5	Q96077
12	165.5	18.3	170	5	Q96077
13	165.5	18.3	195	5	Q96077
14	164.5	18.2	213	5	Q96077
15	163.5	18.1	170	5	Q96077
16	163	18.0	200	5	Q96077

17	162.5	18.0	115	11	Q99109	Q99109 mus musculus
18	162	17.9	274	10	Q9AWM4	Q9AWM4 oryza sativa
19	159.5	17.6	213	10	Q9L7B8	Q9L7B8 arabidopsis
20	157.5	17.4	175	3	Q9HDE1	Q9HDE1 cryptosporidium
21	157.5	17.3	226	10	Q81446	Q81446 arabidopsis
22	156.5	17.1	170	4	Q8WV74	Q8WV74 homo sapien
23	155	17.1	173	4	Q96LZ3	Q96LZ3 homo sapien
24	155	16.8	161	5	Q9AV39	Q9AV39 oryza sativa
25	151.5	16.8	187	5	Q9VW88	Q9VW88 drosophila
26	151.5	16.5	189	5	Q9VNF9	Q9VNF9 drosophila
27	149.5	16.5	192	10	Q81328	Q81328 arabidopsis
28	146	16.2	225	10	Q8W5C8	Q8W5C8 oryza sativa
29	146	16.2	225	10	Q8W5C8	Q8W5C8 oryza sativa
30	144.5	16.0	226	10	Q81447	Q81447 arabidopsis
31	143	15.8	190	3	Q96X50	Q96X50 magnaporthe
32	143	15.8	190	3	Q8TGC0	Q8TGC0 magnaporthe
33	142	15.7	196	5	Q9N2Y1	Q9N2Y1 caenorhabditis
34	142	15.7	246	10	Q82641	Q82641 arabidopsis
35	140.5	15.5	213	10	Q81445	Q81445 arabidopsis
36	140	15.5	229	11	Q930Y5	Q930Y5 mus musculus
37	138	15.3	190	5	Q9NAY9	Q9NAY9 naegleria f
38	137	15.2	214	11	Q9F0Q7	Q9F0Q7 arabidopsis
39	137	15.2	214	11	Q8VCN1	Q8VCN1 mus musculus
40	137	15.2	224	10	Q9SGW7	Q9SGW7 arabidopsis
41	136	15.0	222	10	Q81223	Q81223 trichomonas
42	134.5	14.9	153	5	Q9U5J0	Q9U5J0 trichomonas
43	134.5	14.9	160	5	Q9U5J9	Q9U5J9 homo sapien
44	131	14.5	216	4	Q9NWT9	Q9NWT9 homo sapien
45	129	14.3	191	4	Q9UM19	Q9UM19 homo sapien

ALIGNMENTS

RESULT 1

Q93640 PRELIMINARY; PRT; 311 AA.

AC Q93640; 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE F30A10.1 protein.

GN F30A10.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae.

OC Rhabditidae; Peloderae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN (1)

RP SEQUENCE FROM N.A.

RA Barlow R.

RL Submitted (OCR-1996) to the EMBL/GenBank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology."

RT Science 282:2012-2018(1998).

DR EMBL; 281072; CAB03019.1; .

DR HSSP; Q98828; IDGV.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; efhand; 3.

DR Prodom; PD000012; EF-hand; 1.

DR SMART; SM0054; Efh; 2.

SO SEQUENCE 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;

Query Match 43.5%; Score 393; DB 5; Length 311;

Best Local Similarity 39.6%; Pred. No. 4,1e-24;

Matches 82; Conservative 52; Mismatches 47; Indels 26; Gaps 5;

QY 1 MGGSGSRSLKELLAEYQDLTFLKROELLAAHRRPCCLLPQEQRTVESS 48

DB 111 MGNNASSLSELNLFSGKGVFTREQDEYDCFTFRKDIIRLYKRYALNPKR---VPTN 167

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Db      68 DRICRVSHD---NVSEFDVLGMASVFSEQACPSLKTEYAFRIYDFNENGFIQDEEDLEE 124
QY     131 LVNLCTGEGEDTRLGASE--MKQLIDNIIEESDIDRDGTINLSEFQHVISRSPDFASSFK 188
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     125 IVLRLL-KSDD---ASEDLLMDVHVHVLSESDLDNSMLSFSEFEHAMAKSPDFMNSFR 179
QY     189 I 189
       |
Db     180 I 180

RESULT 3
Q96Q77 PRELIMINARY; PRT; 187 AA.
AC Q96Q77;
ID Q96Q77;
AD Q96Q77;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE KIP3.
DE KIP3.
DE KIP3.
GN KIP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; -
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayashi A., Okaze H., Kozuma S., Saito T.;
RL "KIP3.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB050868; BAB71789.1; -.
DR InterPro; IPRO02048; EF-hand.
DR Pfam; PF00036; efhnd; 3.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF-HAND; UNKNOWN.2.
SQ SEQUENCE 187 AA; 21801 MW; FB32CCB46DF5ADCF CRC64;

Query Match 37.3%; Score 337; DB 4; Length 187;
Best Local Similarity 37.3%; Pred. No. 8.3e-20;
Matches 72; Conservative 52; Mismatches 57; Indels 12; Gaps

QY 1 MGSGSLSKELLAEYQDITFTLTKQIBILLAHRRFCCLLPQ----EORTVESLSRAQVPPE 56
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MGNNQTFFTHEQELENQDCFTTFRKEIKMLFRYQDLAPQLVPLDYTCPD---VKVPYE 57
QY 57 QILSLPELKANPKERICRVFSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 LIGSMPELKNPPQRIAQVES-EDCGHTMLDNFLDMFSVMSEMAPROLKAYYAFKIYD 116
QY 117 XXXXXXXXXXSRLVNLTGEGEDTRLGASEMKQIIDLIESDIDRDGTINLSEFOHV 176
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 FNNDYTICAWDLQTVTKLTRGG----LSAEEVSVCERKVLDEADGDHGRLSLEDQNM 172
QY 177 ISRSPOPASSFKI 189
    | | | | | | | | | |
Db 173 ILRAPDFLSTFHI 185

RESULT 4
Q9WZQ5 PRELIMINARY; PRT; 206 AA.
AC Q9WZQ5;
ID Q9WZQ5;
AD Q9WZQ5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C92236 protein.
DE C92236.
GN C92236.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phryganea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyraoridae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
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RC  SPRAIN-BERKELEY;
RX  MEDLINE-20196006; PubMed-10731132;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amandlides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA  Abill J.F., Agdayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA  Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Bence P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA  Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA  Burrill K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA  Fostler C., Gablelian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodex A., Gong F., Gottell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA  Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA  Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Mlshina N.V., Modyarty C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA  Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spleer E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
DR  EMBL: AB003452; AAF4635.1; -.
DR  HSSP: Q99828; IDGV.
DR  FLYBase: FBgn0034558; CG9236.
DR  InterPro: IPR002048; EF-hand.
DR  Pfam: PF000036; ehand; 3.
DR  ProDom: PD000012; EF-hand; 1.
DR  SMART: SM00054; EFh; 3.
DR  PROSITE: PS00018; EF_HAND; 2.
KW  Calcium-binding.
SQ  SEQUENCE 206 AA; 23591 MW; B3105F7F70F475A9 CRC64;

Query Match      35.5%; Score 320.5; DB 5; Length 206;
Best Local Similarity 40.9%; Pred. No. 2.2e-18;
Matches 72; Conservative 41; Mismatches 46; Indels 17; Gaps 5;

OY  17 QDLFTLTKOELLAHRRFCELLPQ---EORTVESSLRAOVPPFQQLSLBELKANPKRNI 73
DB  43 KDCFTFKREILRVKRFELRPDLVPRMTEGQASVAVPECCIKKMELR----- 94
OY  74 CAVSTSPAKDSLSEDFDLILSVSDTAPDKSHYARIFKXXXXXXXSRLYN 133
DB  95 -EAFSRD-GQGNI,SEDFIDALVSSEQAPRDIKVYARKIVDFDQDGGTIGNAD--LMS 149
OY  134 CLTGEDEPTLSASEMKOLINDILESDIDRCGTINLSFOVIVISSPPFASFKI 189
DB  150 CLTTWTKN-ELSPEDHQIADKIVIEADVDGCKLSILEFHYILRAPDLSTFHI 204

RESULT 5
O9GLJ2      PRELIMINARY;      PRT;      54 AA.
AC  O9GLJ2;
DT  01-MAR-2001 (TREMBlrel. 16, Created)

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DT  01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  DNA-PK interaction-like protein (Fragment).
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Smith T.F.L., Fahrenkug S.C., Rohrer G.A., Simmen F.A.,
RA  Rexroad C.E. III, Keele J.W.;
RT  "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT  cDNA library.";
RL  Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL: A8267715; AAG25931.1; -.
DR  HSSP: Q99828; IDGV.
DR  InterPro: IPR002048; EF-hand.
DR  Pfam: PF000036; ehand; 1.
DR  ProDom: PD000012; EF-hand; 1.
DR  PROSITE: PS00018; EF_HAND; UNKNOWN_1.
FT  NON_TER 1 54
FT  NON_TER 1 54
SQ  SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

Query Match      24.2%; Score 219; DB 6; Length 54;
Best Local Similarity 74.1%; Pred. No. 7.5e-11;
Matches 40; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

OY  102 ATPDIKSHVAFRIFFXXXXXXXXXXSRLYNCLTGEDEPTLSASEMKOLIDN 155
DB  1 ATPDIKSHVAFRIFFDDDDGTLNRDLSQLVNLTEGDEPTLSASEMKOLIDN 54

RESULT 6
O9GP83      PRELIMINARY;      PRT;      180 AA.
ID  O9GP83;
AC  O9GP83;
DT  01-MAR-2001 (TREMBlrel. 16, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  Calcineurin B.
GN  CNBA.
OS  Dictyostellium discoideum (Slime mold).
OC  Eukaryota; Mycetozoa; Dictyostelidae; Dictyostellium.
OX  NCBI_TaxID=44689;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Alchem A.;
RA  Theiss (2000), Department of Fachbereich Biologie,
RA  Universitaet Konstanz, Konstanz, Germany.
RL  [2]
RP  SEQUENCE FROM N.A.
RA  Alchem A.;
RA  STRAIN-AX-2;
RA  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AJ301668; CAC20026.2; -.
DR  HSSP: P06705; IAU1.
DR  InterPro: IPR002048; EF-hand.
DR  InterPro: IPR001125; Recoverin.
DR  Pfam: PF000036; ehand; 4.
DR  PRINTS: PR00450; RECOVERIN.
DR  ProDom: PD000012; EF-hand; 2.
DR  SMART: SM00054; EFh; 4.
DR  PROSITE: PS00018; EF_HAND; UNKNOWN_3.
SQ  SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

Query Match      23.7%; Score 214.5; DB 5; Length 180;
Best Local Similarity 27.0%; Pred. No. 1.1e-09;
Matches 48; Conservative 54; Mismatches 61; Indels 15; Gaps 4;

OY  1 MGGSGSRLSKELLAEYQDITFLTKOELLAHRRFCELLPQDEORTVESSLRAOVPPFQQLS 60

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Db 1 MGQHSLLNKEQLEQKONSFSSEALKKLYRRFQMLDKDGSGLTT-----DEFLS 52
QY 61 LPELKNPFKERICRVFSTSPAKDS-LSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXX 119
Db 53 IPDLALNPLLRVIFQDQ--KDNIEFSEFVGTLATLSHKTKEDKLFQIYDIDC 110
QY 120 XXXXXXXXSRVNCILGTGEGDTRLSASMKOLIDNILEESDIDRGTINLSEFQHV 177
Db 111 DGFISNGELFQVKKMVG-----TNLNDVQLQIIVDKTIIEGDDYDKGKISDFEFHMI 164

RESULT 7
Q93VF2 PRELIMINARY; PRT; 175 AA.
AC Q93VF2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calcineurin-like protein.
GN ECCL1 OR ECCL1.
OS Eucalyptus camaldulensis (Murray red gum), and
OS Eucalyptus grandis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.
OX NCBI_TaxID=34316, 71139;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;
RA Fairbairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197334; AAL25650.1; -.
DR EMBL; AF197330; AAL25647.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF-HAND; UNKNOWN_1.
SQ SEQUENCE 175 AA; 19997 MW; C4E773EE42A3EF16 CRC64;

Query Match 20.6%; Score 186; DB 10; Length 175;
Best Local Similarity 24.2%; Pred. No. 2.5e-07;
Matches 44; Conservative 54; Mismatches 64; Indels 20; Gaps 4;

QY 1 MGGSGRLSKELLAEOYD--LTFLTQKELLHAHRRFCCLLPQQRVTESSLRQVPEQI 58
Db 1 MGNASSMLTYDIEEVQDHCNNLFSQOEIVSLYERFQCL-----DRNAKGFISADEF 52
QY 59 LSLPELKNPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFXXX 118
Db 53 LSVPEFAMNPLSORLLKMW-----DGLNFKDFVAFLSAFSAKASQKQKLELIFKVDSD 106
QY 119 XXXXXXXXSRVNCILGTGEGDTRLSASEMKQIDNILEESDIDRGTINLSEFQHV 178
Db 107 CNGKVSFNIDLEVRDLSG-----PFMSDEQREQLVQVLAEGYTRSYLLDLDVFKVFG 162
QY 179 RS 180
Db 163 NS 164

RESULT 8
Q9LS47 PRELIMINARY; PRT; 175 AA.
AC Q9LS47;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like
DE protein (Hypothetical 20.0 kDa protein).
GN AT3G18430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At3g18430 (GI:15229640).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Sakurai T., Shinn P.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026558; BAB01109.1; -.
DR EMBL; AY063789; AAL36096.1; -.
DR EMBL; AY091287; AAM14226.1; -.
DR HSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF-HAND; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 20.6%; Score 186; DB 10; Length 175;
Best Local Similarity 25.0%; Pred. No. 2.5e-07;
Matches 46; Conservative 53; Mismatches 61; Indels 24; Gaps 5;

QY 1 MGGSGRLSKELLAEOYD--LTFLTQKELLHAHRRFCCLLPQQRVTESSLRQVPE 56
Db 1 MGNSSMLTYDIEEVQSHCHDL--FEQOEILSYLQRFQCL-----DRNAKGFISAD 50
QY 57 QILSLPELKNPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFF 116
Db 51 EFLSVPEFAMNPLSORLLKMW-----DGLNFKDFVAFLSAFSAKASLRQKVLKIFYD 104
QY 117 XXXXXXXXSRVNCILGTGEGDTRLSASEMKQIDNILEESDIDRGTINLSEFQHV 176
Db 105 SDCNGKVSFKDIMEVRLDSG-----SFMSSDQREQLVQVLAEGYTRSYLLDLDVFKI 160
QY 177 ISRS 180
Db 161 FGSS 164

RESULT 9
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Q9U0X7
ID Q9U0X7 PRELIMINARY; PRT; 175 AA.
AC Q9U0X7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcineurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Tosato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,
RA Rajadream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL133435; CAB62809.1; -.
DR HSSP; P06705; 1AUT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.2.
SQ SEQUENCE 175 AA; 19660 MW; 9448F127F4DFA0EB CRC64;

Query Match 20.4%; Score 184; DB 5; Length 175;
Best Local Similarity 22.5%; Pred. No. 3,6e-07;
Matches 41; Conservative 54; Mismatches 73; Indels 14; Gaps 4;

QY 8 LSKELLAAYODLFTFNOEILLARRECELLPOQRTVSSLRQAVPEQIILSPETKAN 67
DB 6 LTAEEIIONINRESTATDAQVRLYKSFSL-----NKDKSGKITRAEFNSIPALASN 57
QY 68 PFAERICRVSTSPAKSLSFEDFDLISVFSPTATPDIKSHVAFRIYXXXXXXX 127
DB 58 PLVDRYLAAMDTD-GDSYVDFGDFRALVALSATSKEDKIRTFKMYDVGDRISNKD 116
QY 128 XSLVNCITGEGEDTRLASSEMKOLINILESDIDRGTINLSEFOVISRSPDFASSF 187
DB 117 LFGMLSTMVG-----VNLSONQLOQIVDKTIFADVDKRGDTTFEERFQ-ALAVNSDFGRRL 171
QY 188 KI 189
DB 172 NL 173

RESULT 10
Q9NFN1 PRELIMINARY; PRT; 169 AA.
AC Q9NFN1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcineurin B.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=20520966; PubMed=11071287;
RX Mecozzi B., Rossi A., Lazaretti P., Kady M., Kaiser S., Valle C.,

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RA C1011 D., Klinkert M.O.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT immunolocalization to the excretory system.";
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1; -.
DR HSSP; P06705; 1NCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.4.
SQ SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match 18.8%; Score 169.5; DB 5; Length 169;
Best Local Similarity 26.0%; Pred. No. 5.4e-06;
Matches 32; Conservative 42; Mismatches 44; Indels 5; Gaps 2;

QY 56 EQLISPELKANPFAERICRVSTSPAKSLSFEDFDLISVFSPTATPDIKSHVAFRI 115
DB 40 KEFSLPELQONPLVARYIEFDYD-GNGEDYFEFIQMSQFSKGEKALFAFRY 98
QY 116 XXXXXXXXXXXXSLVNCITGEGEDTRLASSEMKOLINILESDIDRGTINLSEFOH 175
DB 99 DMDKDGYSNGLFQVLMKMGV---NWLKDTQLQIYDKTIMPPDKRQDGRISPERCE 154
QY 176 VTS 178
DB 155 VVS 157

RESULT 11
Q20804 PRELIMINARY; PRT; 244 AA.
AC Q20804;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE F53C10.1 protein.
GN F53C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderiinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z74036; CAA98489.2; -.
DR HSSP; P06705; 1AUT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.4.
SQ SEQUENCE 244 AA; 27901 MW; 6B99C858CB77D08B CRC64;

Query Match 18.8%; Score 169.5; DB 5; Length 244;
Best Local Similarity 25.0%; Pred. No. 9.5e-06;
Matches 45; Conservative 48; Mismatches 64; Indels 23; Gaps 6;

QY 3 GSGSLSKELLAAYO--DLFTFNOEILLARRECELLPOQRTVSSLRQAVPEQIILS 60
|:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|

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Db 75 GADASLPWEMCSNFDAYELRRLT-----RRFKKL-----DVDGS--GSLSVVEEWS 118
QY 61 LPFLKANPFERICKRVCSTSPAKDSLSFEDFLDLISVFSPTA'PDKSHYAFRIFXXXX 120
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 119 LPFLQNPVLRVTDIED-EDNGEVDVFRFIGIGISQFSVKGDKNTKLKFAFIYDMRD 177
QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLDNILESIDRDGTINLSEFQHVSSR 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GFISNGELFQVLKMWG-----NNLKDSQLQIYDKTILFHDKDGDGKISQFECDVVEHT 233

RESULT 12
Q9NKKW7 PRELIMINARY; PRT; 170 AA.
AC Q9NKKW7
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Calciineurin B.
OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidae; Pectinidae; Mizuhopecten.
ON NCBI_TaxID=6573;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;
RT "Molecular Cloning of cDNA Encoding Two Subunits of Calciineurin from
RT Scallop Testis: Demonstration of Stage-Specific Expression during
RL Maturation of the Testis.";
RL J. Biochem. 0:0-0;(2000);
DR EMBL; AB041524; BAA94543.1; -.
DR HSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;
SQ

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Query Match      18.3%; Score 165.5; DB 5; Length 170;
Best Local Similarity 22.3%; Pred. No. 1.2e-05;
Matches 39; Conservative 52; Mismatches 65; Indels 19; Gaps 4;

QY 3 GSGSLSKELLAAYQDLFLFKQETLLAHRFPCELLPOETRVESSLRAQVPFFQILSLP 62
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 2 GNENSLPWECLSNFD-----PDEIKRLGRF-----RKLLDNGSLVDEFWTLP 47

QY 63 ELKANPFERICRVFSTSPAKDSLSFDFLLLSVFSDTATPDTKSHYAFRIFXXXXXX 122
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 48 ELQQNPLVQRVIDIFDID-NGNEVDFNEFIQGVQSVKQKLSKLSFAFIYDMQDGY 106

QY 123 XXXXXXSLVNCVLGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSFQHV 177
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 107 ISNGELFQVLKMWVG-----NNLKDTLQQIVDKTIIHADADGGCKISFEFCAVV 157

RESULT 13
Q23643
ID Q23643 PRELIMINARY; PRT; 195 AA.
AC Q23643;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE ZK856.8 protein.
GN ZK856.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]

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RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
   investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z70783; CAA94856.1; -
DR HSSP; P06705; IAU1.
DR DRIPPro; IPRO02048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SMO0054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 195 AA; 22670 MW; 9F4FD6D8BD7BA88 CRC64;

Query Match      18.3%; Score 165.5; DB 5; Length 195;
Best Local Similarity 22.3%; Pred.No.1.4e-05;
Matches 44; Conservative 53; Mismatches 69; Indels 31; Gaps 6;

QY 1 MGSGS-RLSKELLAEQDLFTLTKEIILAHRRFCCELLPQEORTVESSLRAQVPFFQIL 59
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 60 SLPELKANPFKRCRVSTSPA-----KDSLFEDFLDLLSVSDTATPDIKSH--- 109
Db ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 53 NVPELVNPLGIRDVADPFTLASSNGDEEQLNQRFVRIHAHFOISR--VKKNALNS 110
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 110 -----YAERIFEXXXXXXXXXXXSRVLNCLTGEGDTPLSASEMKQIDNTLESDD 163
Db ||||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 RKDKLLFAFKMYDUNKNDIITREEFKVLNSMVG----ANITSQDLKIADRTEEDAD 166
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 164 RQGTINLSFEHQHVISRS 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 RDGKISDFCRANEKT 183
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
O16343 PRELIMINARY; PRT; 213 AA.
AC O16343;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE F59D6.7 protein.
GN F59D6.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-94150718; PubMed-7906399;
RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R., Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
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RA Bradshaw H., Graves T.;
RT "The sequence of C. elegans cosmid F53D6."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016435; AAB65882.1;
DR HSSP; P06705; 1AUT.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR Prodom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.2.
SQ SEQUENCE 213 AA; 24432 MW; AB13689122E91391 CRC64;

Query Match 18.2%; Score 164.5; DB 5; Length 213;
Best Local Similarity 22.1%; Pred. No. 2e-05;
Matches 47; Conservative 53; Mismatches 68; Indels 45; Gaps 7;

OY 1 MGSGSRL-----SKELAEYQ-----DLFLTKOELLAHRRFCCLLPQE 41
DB 1 MENSNSIISDAEMREIMDETQCKVIAKQFTPRNTISVNHQILRLRYTRFASL---- 56
OY 42 QRTVESSLRAQVPEQILSLPELKANPFRKICRVSTSPAKD-----SLSPEDLDLL 95
DB 57 ----DKNGGYSRLDDELAVPELAVPLDRIIDAFITLSDSGDSKSGCLTFRQFVRL 112
OY 96 SVF-----SDRATPDIKS--HYAFRIFYXXXXXXXSLVNLGEGEDTRLAS 147
DB 113 AHFQISKYKDNALNSRKDKLRFAPKMYDLNNNYITREPFKYLNSVNG----ANITSD 168
OY 148 EMKOLIDNLEESDIDROGTINLSEFOHYSRS 180
DB 169 QLDKTDADTLEADQDROGKISFEDFCRAMEXT 201

RESULT 15
O95P81
AC O95P81. PRELIMINARY; PRT; 170 AA.
DT 01-DEC-2001 (TREMblrel. 19, Created).
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update).
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Calcineurin B.
CN CNE.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHUKO X RYUAKU; TISSUE-PHEROMONE GLAND;
RA Yoshida T.; Matsumoto S.;
RT "cDNA cloning of heterosubunits of calcineurin from pheromone gland of
RT Bombyx mori."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF287251; AAK83039.1;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR Prodom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.4.
SQ SEQUENCE 170 AA; 19357 MW; SECC15B820097130 CRC64;

Query Match 18.1%; Score 163.5; DB 5; Length 170;
Best Local Similarity 21.9%; Pred. No. 1.7e-05;
Matches 39; Conservative 53; Mismatches 67; Indels 19; Gaps 4;

OY 3 GSGSRLSKELAEYQDLFLTKOELLAHRRFCCLLPQERTVESSLRAQVPEQILSLP 62
DB 2 GNENSIMPELCSNFD-----ADEIRRLGKRF-----RKLDIDNSGALSIDFMSLP 47

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OY 63 ELKANPFRKICRVSTSPAKDISFEDLDLLSVESDTPAPDIKSHYAFRIFYXXXXXX 122
DB 48 ELQONPLVQRYVIDIFD-ADNGEVDPEKEFTQGVQSFSVKGDKLSKLRFARIVDMNDGF 106
OY 123 XXXXXXSLVNLGEGEDTRLASSEMKOLIDNLEESDIDROGTINLSEFOHYSRS 180
DB 107 ISNGELQVLMKMYG-----NNLKDQTLQQLVDTITLFPADKDEGKISFEFCNVYGMT 160

Search completed: January 17, 2003, 12:51:54
Job time : 32 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:03 ; Search time 13 Seconds

(Without alignments)
609.383 Million cell updates/sec

Title: MUT127

Perfect score: 1 MGSGSGRLSKELLAERYDLT.....EFQHVISRSPDFASSKIVL 191

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	955	99.8	191	1	KIP1_HUMAN
2	902	94.3	191	1	KIP1_MOUSE
3	901	94.1	191	1	KIP1_RAT
4	338	35.3	187	1	KIP2_MOUSE
5	336	35.1	187	1	KIP2_HUMAN
6	213.5	22.3	177	1	CALB_NAEGR
7	207.5	21.7	174	1	CALB_SCHPO
8	196.5	20.5	174	1	CALB_NEUCR
9	186.5	20.5	174	1	CALB_YEAST
10	183.5	19.2	169	1	CALB_HUMAN
11	183.5	19.2	169	1	CALB_MOUSE
12	175.5	18.3	170	1	CALC_DROME
13	175	18.3	194	1	CA22_MOUSE
14	171.5	17.9	170	1	CALB_DROME
15	170	17.8	194	1	CA22_HUMAN
16	169.5	17.7	178	1	CALC_MOUSE
17	168.5	17.6	186	1	FRRD_DROME
18	167.5	17.5	175	1	CALC_RAT
19	163.5	17.1	189	1	NC52_CAEEL
20	155	16.2	190	1	APLC_APLCA
21	149.5	15.6	195	1	H520_HUMAN
22	148	15.5	189	1	NC51_HUMAN
23	148	15.5	189	1	NC51_XENLA
24	143	14.9	190	1	NC51_CAEEL
25	143	14.9	192	1	VIS3_CHICK
26	143	14.9	192	1	VIS3_MOUSE
27	142	14.8	192	1	VIS3_HUMAN
28	137	14.3	189	1	NC4H_DROME
29	134	14.0	190	1	VIS2_RAT
30	133.5	13.9	214	1	TESC_HUMAN
31	133	13.9	192	1	NCAD_MOUSE
32	132	13.8	192	1	HIPR_HUMAN
33	128.5	13.4	172	1	CATR_MOUSE

34	128	13.4	192	1	NCAD_CHICK	012953 gallus gall
35	128	13.4	214	1	TESC_MOUSE	091k15 mus musculu
36	127	13.3	192	1	NCAD_HUMAN	P29554 homo sapien
37	127	13.3	192	1	NECX_APLCA	Q16982 aplysia cal
38	127	13.3	791	1	KDGG_HUMAN	P49619 homo sapien
39	126	13.2	189	1	NC51_SCHPO	009721 schizosacch
40	125.5	13.1	172	1	CATF2_HUMAN	Q12798 homo sapien
41	125	13.1	190	1	VIS1_HUMAN	P28677 homo sapien
42	125	13.1	804	1	KDGB_HUMAN	09y6t7 homo sapien
43	123.5	12.9	195	1	H520_MOUSE	09d869 mus musculu
44	121.5	12.7	801	1	KDGB_RAT	P49621 rattus norv
45	121	12.6	189	1	NC51_YEAST	Q06389 saccharomyc

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN STANDARD; PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96054;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (SNK
DE CIB1 OR PRKDCIP OR KIP OR CIB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RA MEDLINE-98040126; PubMed-9372844;
RT Wu X., Lieber M.R.;
RL "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RA TISSUE-Fetal liver;
RL MEDLINE-97184102; PubMed-9030514;
RA Naik U.P., Patel P.M., Parise L.V.;
RL "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RA SEQUENCE FROM N.A.
RL MEDLINE-20284952; PubMed-10826701;
RA Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RL "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP)."
RL DNA Seq. 10:415-418(2000).
RN [5]
RA SEQUENCE FROM N.A.
RL TISSUE-Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RA STRUCTURE BY NMR OF 9-191.
RL MEDLINE-20283154; PubMed-10822252;
RA Hwang P.M., Vogel H.J.;
RL "Structures of the platelet calcium- and integrin-binding protein and
RT the alpha1b-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition: homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
CC 1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC -----
CC EMBL; U83236; AAB39758.1; 1
CC EMBL; U85611; AAB53387.1; 1
CC EMBL; U82226; AAC51106.1; 1
CC EMBL; AB021866; BAA36281.1; 1
CC EMBL; BC000846; AAH00846.1; 1
CC EMBL; IDGV; 08-DEC-99
CC GenBank; HGNC:16920; CIB1.
CC MIM; 602293; 1
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 2.
CC ProDom; PD000012; EF-hand; 1.
CC SMART; SM00054; EFh; 2.
CC PROSITE; PS00018; EF HAND; 2.
KW Calcium-binding; Repeat; 3D-structure.
FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
FT CONFLICT 44 44 T -> S (IN REF. 3 AND 5).
SQ SEQUENCE 191 AA; 21717 MW; 9AA6EA7897891E55 CRC64;

Query Match 99.8%; Score 955; DB 1; Length 191;
Best Local Similarity 99.5%; Pred. No. 2.2e-71;
Matches 190; Conservative 0; Mismatches 1; Indels 0;

QY 1 MGGSGSRLSKELLAEYQDLTFLTKQELLAHRRFCELLPQORTVESSLRAQVPEQILS 60
Dd 1 MGGSGSRLSKELLAEYQDLTFLTKQELLAHRRFCELLPQORTVESSLRAQVPEQILS 60
QY 61 LPKANKPKERICKRVFTSPAKSLSPEDFLDLSVFSPTATPDIKSHYAFRIFDQDD 120
Dd 61 LPKANKPKERICKRVFTSPAKSLSPEDFLDLSVFSPTATPDIKSHYAFRIFDQDD 120
QY 121 GTLNEXLSRLVNCITGEGEDTRLSASEMKQLIDNILEESIDRDGTINLSEFQHVIRS 180
Dd 121 GTLNEXLSRLVNCITGEGEDTRLSASEMKQLIDNILEESIDRDGTINLSEFQHVIRS 180
QY 181 PDFASSFKIVL 191
Dd 181 PDFASSFKIVL 191

RESULT 2
KIP1_MOUSE STANDARD; PRT; 191 AA.
AC Q920F4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-Kidney;

RX MEDLINE-99069785; PubMed-9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohhira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization.";
RL J. Hum. Genet. 43:275-277(1998).
RN (2)
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Petal kidney;
RP MEDLINE-9916047; PubMed-10051332;
RX Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene";
RL Mamm. Genome 10:315-317(1999).
RN (3)
RN SEQUENCE FROM N.A.
RP Naik M.U., Naik U.P.;
RP "Cloning and tissue distribution of murine calcium and integrin
RP binding protein, CIB";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN (4)
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RP MEDLINE-21085660; PubMed-11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RN Nature 409:685-690(2001).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC -----
CC EMBL; AB006463; BAA74429.1; 1
CC EMBL; AB017361; BAA36165.1; 1
CC EMBL; AF173010; AAG38960.1; 1
CC EMBL; AF10345; BAB26868.1; 1
CC HSPSP; Q99828; IDGV.
CC MGD; MGI:134418; Cibl.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 2.
CC ProDom; PD000012; EF-hand; 1.

DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF-hand: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 SO SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.3%; Score 902; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 4.8e-67;
 Matches 179; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELAEYDQFLTKQELLAHRRFCELLPOEORTVESSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELAEYDQFLTKQELLAHRRFCELLPPQRTVESSLHRRVSEFQILS 60
 QY 61 LPELKANPFKRICVSTSPKDSLSFEDFLDLVSFSDPATPDIKSHVAFRIEDFDD 120
 DB 61 LPELKANPFKRICVSTSPKDSLSFEDFLDLVSFSDPATPDIKSHVAFRIEDFDD 120
 QY 121 GTLREXLSRLVNCITGEGEDTRLASSEMKNOLINDIESDIDRGTINLSEFQHVIRS 180
 DB 121 GTLREXLSRLVNCITGEGEDTRLASSEMKNOLINDIESDIDRGTINLSEFQHVIRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 RA Scatoldi J., Staubli U., Bereliter-Hahn J., Streibhardt K., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).

- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC - SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC - SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL: AF136585; AAF08368.1;
 DR HSSP: Q99828; IDGV.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 DR ProDom: PD000012; EF-hand; 1.

DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF-hand: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 SO SEQUENCE 191 AA; 21800 MW; 3B00B0228879EC7 CRC64;

Query Match 94.1%; Score 901; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 5.8e-67;
 Matches 179; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELAEYDQFLTKQELLAHRRFCELLPOEORTVESSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELAEYDQFLTKQELLAHRRFCELLPPQRTVESSLHRRVSEFQILS 60
 QY 61 LPELKANPFKRICVSTSPKDSLSFEDFLDLVSFSDPATPDIKSHVAFRIEDFDD 120
 DB 61 LPELKANPFKRICVSTSPKDSLSFEDFLDLVSFSDPATPDIKSHVAFRIEDFDD 120
 QY 121 GTLREXLSRLVNCITGEGEDTRLASSEMKNOLINDIESDIDRGTINLSEFQHVIRS 180
 DB 121 GTLREXLSRLVNCITGEGEDTRLASSEMKNOLINDIESDIDRGTINLSEFQHVIRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (Kip 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Testis;
 RX MEDLINE-99132027; PubMed-9931475;
 RA Selt N., Hattori A., Hayashi A., Kosuma S., Ohira M., Hori T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 RT of DNA-PKcs interacting protein (Kip) gene.";
 RL Biochim. Biophys. Acta 1444:143-147(1999).
 CC - SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: AB01680; BAA36545.1;
 DR HSSP: Q99828; IDGV.
 DR MGD: MGI:1929293; KIP2.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 3.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF-hand: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 157 168
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBDB0B6F5C CRC64;

Query Match 35.3%; Score 338; DB 1; Length 187;
 Best Local Similarity 37.3%; Pred. No. 5.7e-21;
 Matches 72; Conservative 43; Mismatches 66; Indels 12; Gaps 4;

QY 1 MGGSGSLSKELLAAYQDLTFLTKQELLAAHRRFCE-----LLPQEQRTVSSLRQVPE 56
 DB 1 MGNQTIPTFEQLDNYQDCTFFNKKDILKLSRFLYELAPNLVPMYDR---KSPIVHVPM 57
 QY 57 QILSPELKANPFKRICRVSTSPAKDSLSFEDFLDLSVFSOTATPDIKSHYAFRIFD 116
 DB 58 LIQMPLELRNPFKRICRVSTSPAKDSLSFEDFLDLSVFSOTATPDIKSHYAFRIFD 116
 QY 117 FDDGTLNREXLSRLVNLCTGEGEDTRLSASEMKOLIDNILEESIDRDGTINLSEFQHV 176
 DB 117 FNTDNFKCKEDLEMTLARLT---KSELEDEEVVLVCDKVEEADLDGDKGLGFADFEDM 172
 QY 177 ISRSPDFASSPKI 189
 DB 173 IAKAPDFLSTPHI 185

RESULT 5
 KIP2_HUMAN STANDARD; PRT; 187 AA.
 AC 075838;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RA MEDLINE=9913207; PubMed=9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 of DNA-PKcs interacting protein (KIP) gene.";
 RL Blochm. Biophys. Acta 1444:143-147(1999).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
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 CC
 CC EMBL; AB012955; BAA33584.1; -
 CC HSPSP; Q99828; IDGV.
 CC MIM; 605564;
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; ehand; 3.
 CC ProDom; PD000012; EF-hand; 1.
 CC SMART; SM00054; EFH; 2.
 CC PROSITE; PS00018; EF_HAND; 2.
 CC Calcium-binding; Repeat.
 CC CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 CC CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
 CC SEQUENCE 187 AA; 21643 MW; D51F6C25AD381BEF CRC64;

Query Match 35.1%; Score 336; DB 1; Length 187;
 Best Local Similarity 37.3%; Pred. No. 8.3e-21;
 Matches 72; Conservative 43; Mismatches 66; Indels 12; Gaps 4;

QY 1 MGGSGSLSKELLAAYQDLTFLTKQELLAAHRRFCE-----LLPQEQRTVSSLRQVPE 56
 DB 1 MGNQTIPTFEQLDNYQDCTFFNKKDILKLSRFLYELAPNLVPMYDR---KSPIVHVPM 57
 QY 57 QILSPELKANPFKRICRVSTSPAKDSLSFEDFLDLSVFSOTATPDIKSHYAFRIFD 116
 DB 58 LIQMPLELRNPFKRICRVSTSPAKDSLSFEDFLDLSVFSOTATPDIKSHYAFRIFD 116
 QY 117 FDDGTLNREXLSRLVNLCTGEGEDTRLSASEMKOLIDNILEESIDRDGTINLSEFQHV 176
 DB 117 FNTDNFKCKEDLEMTLARLT---KSELEDEEVVLVCDKVEEADLDGDKGLGFADFEDM 172
 QY 177 ISRSPDFASSPKI 189
 DB 173 IAKAPDFLSTPHI 185

RESULT 6
 CALB_NAEGR STANDARD; PRT; 177 AA.
 AC P42322;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
 DE (Calcineurin regulatory subunit).
 GN CNB1.
 OS Naegleria gruberi.
 OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
 OX NCBI_TaxID=5762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEG;
 RX MEDLINE=95172399; PubMed=7867946;
 RA Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;
 RT "A calcineurin-B-encoding gene expressed during differentiation of
 the amoeboid flagellate Naegleria gruberi contains two introns.";
 RL Gene 154:39-45(1995).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY (BY SIMILARITY).
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B) (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC
 CC EMBL; U04380; AAA81896.1; -
 CC HSPSP; P06705; LAUI.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; ehand; 4.
 CC ProDom; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFH; 4.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC Calcium-binding; Repeat.
 CC CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).
 CC CA_BIND 70 81 EF-HAND 2 (BY SIMILARITY).
 CC CA_BIND 107 118 EF-HAND 3 (BY SIMILARITY).
 CC CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).
 CC SEQUENCE 177 AA; 20057 MW; 01D4A48E6947E97C CRC64;

Query Match 22.3%; Score 213.5; DB 1; Length 177;
 Best Local Similarity 29.2%; Pred. No. 7.9e-11;
 Matches 52; Conservative 39; Mismatches 74; Indels 13; Gaps 3;

QY 1 MGGSGSLSKELLAAYQDLTFLTKQELLAAHRRFCELLPQEQRTVSSLRQVPEQILS 60
 DB 1 MGNQTIPTFEQLDNYQDCTFFNKKDILKLSRFLYELAPNLVPMYDR---KSPIVHVPM 57

```

Db      1 MGTTSSRPEEVEEMOKGNTQKIKKLYKRRKKDKDNGTISK-----DEFLM 52
QY      61 LPELKANPFRERICRVSTSPAKDSLFEDFLDLVSFDPATPDIKSHVAFRIEDPDD 120
      53 IPELAVNPLVKRIVSISIDEN-GDGSVNFKEITALSVFNAGDKORKLEEFKRYDIDGD 111
QY      121 GTLNREXLSRLVNCJLGEEDTRLASSEMQLDINIEESDIDRDGTINLSEFQHVIS 178
      112 GYISNGELFVYLMKMGV-----NNLSDVQLQOIVDKTILEADEDDGKISFEFPKRTLS 165

RESULT 7
CALB_SCHPO STANDARD; PRT; 174 AA.
ID      CALB_SCHPO
AC      090U93;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE      (Calcineurin regulatory subunit).
DE      CNB1 OR SPCC830.06.
OS      Schizosaccharomyces pombe (fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC      Schizosaccharomycetales; Schizosaccharomycetaceae;
OC      Schizosaccharomycetes.
OX      NCBI_TaxID=4896;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=972;
RX      MEDLINE=21648401; PubMed=11859360;
      Wood V., Galliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
      Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
      Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
      Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
      Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
      Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
      James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
      Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
      Oliver K., O'Neill S., Pearson D., Quail M.A., Reddington E.,
      Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
      Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
      Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
      Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
      Wellens I., Vanstreels E., Rieger M., Schaefer M., Mellier-ner S.,
      Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
      Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
      Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
      Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
      Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
      Dague R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
      Cerrutti L., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
      Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
      Shpakowski G.V., Usasery D., Barrett B.G., Nurse P.;
      "The genome sequence of Schizosaccharomyces pombe.";
      Nature 415:871-880(2002).
RT      -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
      CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
      SENSITIVITY (BY SIMILARITY).
      -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
      SUBUNIT (B) (BY SIMILARITY).
      -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
      SITES (BY SIMILARITY).
      -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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DR      EMBL: AL109850; CAB52879.1;
DR      HSSP: P06705; 1AU1.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR001125; Recoverin.
DR      Pfam: PF00036; efhand; 4.
DR      PRINTS: PR00450; RECOVERIN.
DR      ProDom: PD000012; EF-hand; 1.
DR      SMART: SM00054; EFh; 4.
DR      PROSITE: PS00018; EF-HAND; 4.
KW      Calcium-binding; Myristate.
FT      CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
FT      CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).
FT      CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
FT      CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).
SQ      SEQUENCE 174 AA; 19675 MW; EEF38FE74959442E CRC64;

Query Match 21.7%; Score 207.5; DB 1; Length 174;
Best Local Similarity 27.2%; Pred. No. 2.4e-10;
Matches 49; Conservative 45; Mismatches 69; Indels 17; Gaps 4;

QY      1 MGSGSRLSRLAEYDGLFLTRQETLLARPCCELLPQQRVTESSLRQVFEQILS 60
      1 MGOSQOIFEDLISN-----SFSNEIEIRIKRRIK-----IDANOGGSIDRNFTLS 48
Db      1 LPELKANPFRERICRVSTSPAKDSLFEDFLDLVSFDPATPDIKSHVAFRIEDPDD 120
QY      61 IPELAVNPLVKRIVSISIDEN-GDGSVNFKEITALSVFNAGDKORKLEEFKRYDIDRD 107
      49 IPELAVNPLVKRIVSISIDEN-GDGSVNFKEITALSVFNAGDKORKLEEFKRYDIDRD 107
Db      121 GTLNREXLSRLVNCJLGEEDTRLASSEMQLDINIEESDIDRDGTINLSEFQHVIS 180
      108 GYISNGELFVYLMKMGV-----TNLRDQLQOIVDKTILEADEDDGKISFEFPKRTLS 163

RESULT 8
CALB_NEUCR STANDARD; PRT; 174 AA.
ID      CALB_NEUCR
AC      P87072; O13408.
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE      (Calcineurin regulatory subunit).
DE      CNB-1 OR CAN-B.
OS      Neurospora crassa.
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Sordariales; Sordariaceae; Neurospora.
OX      NCBI_TaxID=5141;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=74A;
RX      MEDLINE=98007857; PubMed=9349701;
      Prokisch H., Yarden O., Dleminger M., Tropschug M., Barthelmess I.B.;
      "Impairment of calcineurin function in Neurospora crassa reveals its
      essential role in hyphal growth, morphology and maintenance of the
      apical Ca2+ gradient.";
      Mol. Gen. Genet. 256:104-114(1997).
RT      -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
      CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
      SENSITIVITY.
      -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
      SUBUNIT (B).
      -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
      SITES.
      -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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DB 1 GAAPSKIVDGLD-----TFNDEIRLRKRRKIDRDSGSGIDKN-----EFMSI 48

QY 62 PELKANPEKRICRVSTSPAKSLSEDFDLVSFSDTATPDIKSHYAFRIPFDDG 121

DB 49 PGVSNPLAGRIMEVFDADNSGD-VDFQETITGSISSGSGNDEKRAFRAKIDIDKDG 107

QY 122 TLNREKLSLVNLTGEGEETRLSASMKOLIDNILESIDIRDTNLSEFOHYI 177

DB 108 FLSNGELFTYIKIMVG-----SNLDEDELOQIVRTIVENDSDGGRISFEFFKNAI 159

RESULT 10

CALB_HUMAN STANDARD: PRT: 169 AA.

AC P06705; P15117; Q08044;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calneurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1). (Protein phosphatase 3 regulatory subunit B alpha isoform 1).

GN PPP3R1 OR CNB OR CNA2.

OS Homo sapiens (Human).

OS Bos taurus (Bovine), and

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606, 9913, 10116;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES-Human;

RX MEDLINE=90126237; PubMed=2558868;

RA Guenini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;

RT "Isolation and sequence of a cDNA clone for human calneurin B, the

RT phosphatase.";

RT DNA 8:675-682(1989).

RL [2]

RN SEQUENCE FROM N.A.

RP SPECIES-Bovine;

RC Nargang C.E., Bottorff D.A., Adachi K.;

RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-168.

RC SPECIES-Bovine; TISSUE-Brain;

RX MEDLINE=84132092; PubMed=6321184;

RA Aitken A., Klee C.B., Cohen P.;

RT "The structure of the B subunit of calneurin.";

RT Eur. J. Biochem. 139:663-671(1984).

RL [4]

RN SEQUENCE FROM N.A.

RP SPECIES-Rat;

RC Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;

RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC SPECIES-Rat; TISSUE-Brain, and Testis;

RX MEDLINE=94153993; PubMed=8110831;

RA Chang C.-D., Mukai H., Kuno T., Yanaka C.;

RT "cDNA Cloning of an alternatively spliced isoform of the regulatory

RT subunit of Ca2+/calmodulin-dependent protein phosphatase (calneurin

RT B alpha 2).";

RL Biochim. Biophys. Acta 1217:174-180(1994).

RN [6]

RP CALCIUM-BINDING DATA.

RC SPECIES-Bovine;

RX MEDLINE=80101597; PubMed=293720;

RA Klee C.B., Crouch T.H., Krinks M.H.;

RT "Calneurin: a calcium- and calmodulin-binding protein of the

RT nervous system.";

RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RC SPECIES-Bovine;

RX MEDLINE=95360994; PubMed=7543369;

RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.;

RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Nevila M.A.;

RT "X-ray structure of calneurin inhibited by the immunophilin-

RT immunosuppressant, FKBP12-FK506 complex.";

RL Cell 82:507-522(1995).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RC SPECIES-Human;

RX MEDLINE=96097077; PubMed=8524402;

RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.;

RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moosaw E.W.;

RA Castinel L.N., Habuka N., Chen X., Maldonado F., Baker J.E.;

RA Baggett R., Villafraña J.E.;

RT "Crystal structure of human calneurin and the human FKBP12-FK506-

RT calneurin complex.";

RL Nature 378:641-644(1995).

CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,

CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM

CC SENSITIVITY.

CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY

CC SUBUNIT (B).

CC -1- ALTERNATIVE PRODUCTS: 2 ISOBFORMS; 1 (SHOWN HERE) AND 2; ARE

CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.

CC -1- TISSUE SPECIFICITY: ISOBFORM 2 IS TESTIS-SPECIFIC.

CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING

CC SITES.

CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

CC -----

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CC -----

DR EMBL: M30773; AAB08721.1; -

DR EMBL: X71666; CAA50659.1; -

DR EMBL: L03554; AAA40854.1; -

DR EMBL: D14568; BAA03422.1; -

DR EMBL: D14425; BAA03318.1; -

DR PIR: A33391; A33391.

DR PIR: S34127; S34127.

DR PIR: J70297; J70297.

DR PIR: S42716; S42716.

DR PIR: S42717; S42717.

DR PDB: 1AUI; 03-DEC-97.

DR PDB: 1TCO; 12-FEB-97.

DR GeneW: HGNC:9317; PPP3R1.

DR MIM: 601302; -

DR InterPro: IPR002048; EF-hand.

DR Pfam: PF00036; efhand; 4.

DR ProDom: PD000012; EF-hand; 2.

DR SMART: SM00054; EFh; 4.

DR PROSITE: PS00018; EF_HAND; 4.

KW Calcium-binding; Repeat; Alternative splicing; Myristate;

KW 3D-structure.

FT INIT MET 0 0

FT LIPID 1 1

FT CA_BIND 30 41

FT CA_BIND 62 73

FT CA_BIND 99 110

FT CA_BIND 140 151

FT VARSPIC 1 1

FT G -> MEGCTLDQSIFFPTKFNFKKCKDFRQNKTFPSR

FT CONFLICT 11 11

FT CONFLICT 153 153

FT SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 19.2%; Score 183.5; DB 1; Length 169;

Best Local Similarity 31.1%; Pred. No. 2,1e-08;

Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQTLSPKLPKPFKRICRVFSTPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 115
 Db 40 EEFMSLPKLPKPFKRICRVFSTPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 98
 QY 116 DFDDGTLNREKSLRVNCLTGEGETRSLASEMKQLDINLEESDIDRDGTINLSEFOH 175
 Db 99 DMDKGYISNGELFQVLKMMVG---NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 154
 QY 176 VI 177
 Db 155 VV 156

RESULT 11
 CALB_MOUSE
 ID CALB_MOUSE STANDARD; PRT; 169 AA.
 AC Q63810;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
 DE subunit 1).
 GN PPP3R1 OR CNB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92392379; PubMed=1325794;
 RA Ueki K., Muramatsu T., Kincaid R.L.;
 RT "Structure and expression of two isoforms of the murine calmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).";
 RL Biochem. Biophys. Res. Commun. 187:537-543(1992).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONPERS CALCIUM SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC EMBL; S43864; AAB23171.1;
 CC DR HSP; P06705; 1AUI.
 CC DR MGD; MGI:107172; Pp3r1.
 CC DR InterPro; IPR002048; EF-hand.
 CC DR Pfam; PF000036; efhand; 4.
 CC DR ProDom; PD000012; EF-hand; 2.
 CC DR SMART; SM00054; EFh; 4.
 CC DR PROSITE; PS00018; EF-HAND; 4.
 CC KW Calcium-binding; Repeat; Myristate.
 FT INIT-MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY)..
 FT CA_BIND 30 41 EF-HAND 1.
 FT CA_BIND 62 73 EF-HAND 2.
 FT CA_BIND 99 110 EF-HAND 3.
 FT CA_BIND 140 151 EF-HAND 4.
 CC SEQUENCE 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;

Query Match 19.2%; Score 183.5; DB 1; Length 169;
 Best Local Similarity 31.1%; Pred. No. 2.1e-08;
 Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQTLSPKLPKPFKRICRVFSTPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 115
 Db 40 EEFMSLPKLPKPFKRICRVFSTPAKDSLSFEDLLSVFSDTATPDIKSHYAFRI 98
 QY 116 DFDDGTLNREKSLRVNCLTGEGETRSLASEMKQLDINLEESDIDRDGTINLSEFOH 175
 Db 99 DMDKGYISNGELFQVLKMMVG---NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 154
 QY 176 VI 177
 Db 155 VV 156

RESULT 12
 CALC_DROME
 ID CALC_DROME STANDARD; PRT; 170 AA.
 AC Q24214; Q9V315;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcineurin B subunit, isoform 2 (Protein phosphatase 2B regulatory subunit).
 GN CNB2 OR CNB2 OR CG11217.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=97080515; PubMed=8921860;
 RA Warren W.D., Phillips A.M., Howells A.J.;
 RT "Drosophila melanogaster contains both X-linked and autosomal homologues of the gene encoding calcineurin B.";
 RL Gene 177:149-153(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit R.A., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B). THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: NO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U56245; AAC47350.1; -
CC DR EMBL: AE003840; AAF59195.1; ALU_SEQ.
CC DR HSSP: P06705; LTGO.
CC DR Flybase: FBgn0015614; Canb2.
CC DR InterPro: IPR002048; EF-hand.
CC DR InterPro: IPR001125; Recoverin.
CC DR Pfam: PF00036; ehand; 4.
CC DR PRINTS: PR00450; RECOVERIN.
CC DR ProDom: PD000012; EF-hand; 2.
CC DR SMART: SM00054; Eph; 4.
CC DR PROSITE: PS00018; EF_HAND; 4.
CC KW Calcium-binding; Repeat.
CC FT CA_BIND 31 42 EF_HAND 1 (POTENTIAL).
CC FT CA_BIND 63 74 EF_HAND 2 (POTENTIAL).
CC FT CA_BIND 100 111 EF_HAND 3 (POTENTIAL).
CC FT CA_BIND 141 152 EF_HAND 4 (POTENTIAL).
CC SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;
CC
CC Query Match 18.3%; Score 175.5; DB 1; Length 170;
CC Best Local Similarity 24.7%; Pred. No. 9.6e-08;
CC Matches 44; Conservative 42; Mismatches 73; Indels 19; Gaps 4;
CC
CC QY 3 GSGSLKSELLAEYQDLFLFKQELLHARRPCCLLPORIVVSSLRQAQVFEQLISLP 62
CC Db 2 GNETSLPMEKSNFD-----ADEIRLRCKRP-----RLDLDNSGALSVDEKMSGP 47
CC QY 63 ELKAPFERICRVSTSPAKDLSFEFDLILSVFSDPATFDISHTVFRIFDDDDGT 122
CC Db 48 ELQNPPLVQRYVIDFD-ADGNGEVPFKETIQGVSOFSYGVKDLKLRFAFRIDMDNDXY 106
CC QY 123 LNRXLSLVLNQLTGEEDTRLASAEKQILNILEESPIDRDGTLNLSFGHVSRS 180
CC Db 107 ISNGELFEVLKMWG-----NNLKDTQLOQIYDKITGFADKEDGKISDFEFCVAGNT 160
CC
CC RESULT 13
CC CA22_MOUSE STANDARD: PRT: 194 AA.
CC AC 062877;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (sld470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd K.K., Dewitt N.D., Chang A., Mills K.,
RA Sztul E.S.,
RT "A novel Ca²⁺-binding protein, p22, is required for constitutive
RT membrane traffic."
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitkubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.,
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na⁺/H⁺
RT exchanger."
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBD databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Glasi C., Kung B., Kochiva H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata J., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Welt C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection,"
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -1- PFM: BOTH N-ARYSTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -1- SIMILARITY: CONTRAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U39875; AAB04146.1; -
CC DR EMBL: AB070350; BAB63368.1; -
CC EMBL: AB025217; BAA64688.1; -

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DR EMBL: AK005067; BAB23791.1; -
DR HSP; P06705; 1AUI.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF-HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0
FT LIPID 1
FT DOMAIN 38 49 MYRISTATE (PROBABLE).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
FT MUTAGEN 133 133 1E->A: LOSS OF TARGETING/FUSION FUNCTION.
SQ SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 18.3%; Score 175; DB 1; Length 194;
Best Local Similarity 26.8%; Pred. No. 1.2e-07;
Matches 52; Conservative 34; Mismatches 76; Indels 32; Gaps 6;

QY 5 GSR-----LSKELLARYQDLTFTKOEIIAHRFCCELLPQEQRTVSSLRQVPEQILS 60
DB 1 GSRATLLDELEIKKETGSHSQITLYSRFTSLDKGENTLSR-----EDQR 52
QY 61 LPKLANPKERICRVFTSPAKDSLFEDFLDLLSVF-----SDATPD----- 105
DB 53 IPEALNPLGDIINAF-FSEGDQVNRFGFMRTLAHFRPIEDNEKSDVNGPEPLNSRS 111
QY 106 IKSHVAFRFDGDTLNREXLSRLVNCVLCGEEDTRLASSEMQLDNLILESDIRD 165
DB 112 NKLHFAFRFLYDKDKISRLQVLRMWG-----VNISDQLGSIADRTIQEQDQGD 167
QY 166 GTINLSEFOHVSR 179
DB 168 SAISTEFVKVLEK 181

RESULT 14
CALB DROME STANDARD; PRT; 170 AA.
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
DE subunit).
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
[2]
RN SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahle Z., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J.M., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC 1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC 1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC 1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC 1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC
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CC
CC EMBL; M97215; AAA28411.1; -.
CC EMBL; AE003434; AAF46026.1; -.
CC HSSP; P06705; ITCO.
CC FlyBase; FBgn0010014; CanB.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF-HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19341 MW; 77D89BE9D961900 CRC64;

Query Match 17.9%; Score 171.5; DB 1; Length 170;
Best Local Similarity 26.5%; Pred. No. 2e-07;
Matches 41; Conservative 37; Mismatches 64; Indels 13; Gaps 3;

QY 26 ETLAHRFCCELLPQEQRTVSSLRQVPEQILSLPELKANPKERICRVFTSPAKDS 85
DB 19 ETRRIGKRF-----RKLDLDNSCALSIDFMSLPELQQLVQRVIDIFD-ADNGNE 69

```

QY 86 LSEFEDLLSVESDTPDKSHYAFRIFPDGDLNREXLSRLVNCITGEGEDTRL 145
 Db 70 VDFKEFLQVSGSPVSGDKSLRFAFRIDMNDGITSNGELFOVLKAMVG-----NNLK 125
 QY 146 ASMKQLIDNILEESDIDRDGTINLSEFOHVISR 180
 Db 126 DTQLOQIVDKTICFADKDEGKISFDEFCVGN 160

RESULT 15
 CA22_HUMAN STANDARD; PRT; 194 AA.
 AC 099653;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog)
 DE CHP.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X, Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U61538; AAB37770.1;
 DR EMBL; BC001646; AAH01646.1;
 DR HSSP; P06705; IAU1.
 DR MIM; 606988;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; Efh; 2.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 DR Calcium-binding; Repeat; Myristate; Phosphorylation.
 KW INIT_Met 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDESF03C88380 CRC64;
 Query Match 17.8%; Score 170; DB 1; Length 194;
 Best Local Similarity 26.3%; Pred. No. 3.2e-07;
 Matches 51; Conservative 34; Mismatches 77; Indels 32; Gaps 6;
 QY 5 GSR-----LSKLLAEYODLFTFLKOEILLHRRRCCELLPQEQRTVESSLAQVPFGIIS 60
 Db 1 GSRASTLRDDELEIKETGFSHSQITRLYSFTSLDKENGTLNR-----EDFOR 52
 QY 61 LPELKANPEFERICRVFTSPARDSLSEFEDFLDLVYF-----SDTATPD----- 105
 Db 53 IPELAINPLDRIILNFFPE-GEDQVYFRGFMFLHFRIEDNEKSKDVNGEPLNSRS 111
 QY 106 IKSHYAFRIFDEDDGTLNREXLSRLVNCITGEGEDTRLASMKQLIDNILEESDIDRD 165
 Db 112 NKLHFAFRILDLDKDEKISDELLOYLRMMVG-----VNISDEQLGSIADRTIOEADODGD 167
 QY 166 GTINLSEFOHVISR 179
 Db 168 SALSFTPEFVKLEK 181

Search completed: January 17, 2003, 12:42:25
 Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 17 Seconds
(without alignments)
1080.099 Million cell updates/sec

Title: MUT127

Perfect score: 957
Sequence: 1 MGSGSRLSKELAEYODLT.....EFQHYISRPDPASSFKIVL 191

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR-73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	42.4	311	2 T21563	hypothetical prote
2	207.5	21.7	174	2 T41632	probable calcineur
3	201.5	21.1	175	2 JH0462	phosphoprotein pho
4	196.5	20.5	174	2 T47245	calcineurin regula
5	183.5	19.2	170	1 A33391	calcineurin regula
6	183.5	19.2	170	1 S34127	calcineurin regula
7	183.5	19.2	170	1 JCI1220	calcineurin regula
8	183.5	19.2	216	1 S42716	calcineurin regula
9	180.5	18.9	369	2 T22708	hypothetical prote
10	175.5	18.3	170	2 JCI174	calcineurin regula
11	172.5	18.0	170	2 JCI7242	calcineurin regula
12	171.5	17.9	170	2 A44307	calcineurin regula
13	169.5	17.7	179	2 JCI1221	calcineurin regula
14	167.5	17.5	165	2 PS0361	calcineurin regula
15	167.5	17.5	176	2 JQ1232	calcineurin regula
16	167.5	17.5	195	2 T28047	hypothetical prote
17	167.5	17.5	213	2 T31775	hypothetical prote
18	163.5	17.1	190	2 T20725	hypothetical prote
19	161.5	16.9	226	2 T51357	calcineurin B-like
20	153	16.0	190	2 T5186	calcineurin B-like
21	149.5	15.6	226	2 T08923	calcineurin B-like
22	148.5	15.5	213	2 T51356	calcineurin B-like
23	148	15.5	193	2 JH0816	neural vistin-lik
24	148	15.5	24	2 T50676	gene Rem-1 protein
25	148	15.5	246	2 T05308	hypothetical prote
26	148	15.5	246	2 H85387	hypothetical prote
27	147	15.4	193	2 S47565	calcium-binding pr
28	145	15.2	192	2 T01375	calcium sensor hom
29	142	14.8	190	2 A55666	neurocalcin - fru1

30	139	14.5	191	2 JH0815	neural vistin-lik
31	135.5	14.2	254	2 T29566	hypothetical prote
32	135	14.1	193	2 JC2186	hypocalcin - huma
33	135	14.1	270	2 JC7631	K+ channel-interac
34	134	14.0	224	2 F96668	protein PIN1.5 [1
35	132	13.8	193	2 JH0616	neurocalcin (clone
36	132	13.8	195	2 JC1347	hypocalcin - rat
37	131	13.7	190	2 S58303	related to neurona
38	130	13.6	191	2 JH0605	neural vistin-lik
39	130	13.6	191	2 A48979	vistin-lik prote
40	128.5	13.4	172	2 S38531	caltractin - mouse
41	127	13.3	791	2 A53691	diacylglycerol kin
42	126	13.2	190	2 S61168	hypothetical prote
43	125.5	13.1	172	2 I38424	centrin - human
44	124	13.0	214	2 T08922	hypothetical prote
45	123.5	12.9	202	2 S21155	recoverin - mouse

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19442
A/Accession: T21563
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-311 <WIL>
A/Cross-references: EMBL:Z81072; PTDN:CA803019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: clone F30A10
C/Genetics:
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match
Best Local Similarity 42.4%; Score 406; DB 2; Length 311;
Matches 87; Conservativity 41; Mismatches 53; Indels 26; Gaps 5;

QY 1 MGSGSRLS-----KELAEYODLTFLKOEILAHRRFCCLPQEQRTYESS 48
DB 111 MGNMSSSSELNLPKSGVFTREQLDEYQDCTFFTRKDIIRLYRFTALNPHK--VPTN 167
QY 49 LRAQVP-----FEQILSLPELKANPFKERICRVFSTSPAKDLSFEDFDLVSFSDTA 102
DB 168 MGNMFAITTLTFEEVEKPELKEMPRKRCVPS-EDGNGNSPFDLDFMVSFSEMA 226
QY 103 TPDIKSHAFRIIPDDDTGATNREKLSLVNCLGEGEDTFLASSEKMLDITLESDDI 162
DB 227 PLQKLTAFRIYDYGELLGHDLCKMISLTRD----ELSDVEVEFITERIEBADL 282
QY 163 DRDGTINLSEFOYHSRSPDPASSFKI 189
DB 283 DGDSINAFERHYVSRSPDITRTFHI 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R:McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Rampsberger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41632
A/Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-174 <MCD>
A:Cross-references: EMBL:AL109850; PIDN:CAB52879.1; GSPDB:GN00068; SPDB:SPCC830.06
A:Experimental source: strain 972h-; cosmid c830
C:Genetics:
A:Gene: SPDB:SPCC830.06
A:Map position: 3
A:Introns: 18/1; 97/1; 134/3
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 21.7%; Score 207.5; DB 2; Length 174;
Best Local Similarity 27.2%; Pred. No. 1.8e-09;
Matches 49; Conservative 45; Mismatches 69; Indels 17; Gaps 4;

QY 1 MGSGSRLSKELLAEOYTFLTKQCEILLAHRRFCPELLPQEORTVESSLRQAQPFEQILS 60
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MQSQSOIFEDLIEN-----SSFSNEIEIRIKRFK-----IDANQSGSIDRNEFLS 48

QY 61 LPELKAMPKERICRVFSTSPAKDSISDFEDLLLSVFSDTATPDITKSHYAFRIFFDDDD 120
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 49 IPSVASNPPLASRLFVSVDDEGGD-VDFQEFINSLSVFSVHGKKEKLFAFKIYDIRD 107

QY 121 GTLNREXSLVNCLGEGEDTRLSEMKQLINDILESDIDRDGTINLSEFQHVISKS 180
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 108 GTYSNGELYLVLMWVG---TNLRDLOQQIVDKTIMEYDKDRDGKISFEFEKDIVSGS 163

RESULT 3

JH0462
phosphoprotein phosphatase regulatory chain - yeast (Saccharomyces cerevisiae)
N:Alternate names: calcineurin chain B homolog; protein phosphatase 2B chain B; protein C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence.revision 31-Mar-1992 #text.change 20-Jun-2000
C:Accession: JH0462; A45021; S33962; S38022; S38027; S34680; S52282
R:Kuno, T.; Tanaka, H.; Mukai, H.; Chang, C.D.; Hiraga, K.; Miyakawa, T.; Tanaka, C.
Biochem. Biophys. Res. Commun. 180, 1159-1163, 1991
A:Title: cDNA cloning of a calcineurin B homolog in Saccharomyces cerevisiae.
A:Reference number: JH0462; MUID:92062059; PMID:1659397
A:Accession: JH0462

A:Molecule type: mRNA
A:Residues: 1-175 <NU>
A:Cross-references: EMBL:D10293; NID:g218409; PIDN:BAA01136.1; PID:g218410
R:Cyert, M.S.; Thorner, J.
Mol. Cell. Biol. 12, 3460-3469, 1992
A:Title: Regulatory subunit (CNBL gene product) of yeast Ca2+/calmodulin-dependent phosphatase.
A:Reference number: A45021; MUID:92334345; PMID:1321337
A:Accession: A45021
A:Molecule type: DNA
A:Residues: 1-175 <CYE>
A:Cross-references: EMBL:M87508; NID:g171250; PIDN:AAA34505.1; PID:g171251
A>Note: sequence extracted from NCBI backbone (NCBIN:108731, NCBI:P.108732)
R:Cheret, G.; Mattheakis, L.C.; Sor, F.
Feast 9, 661-667, 1993
A:Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cerevisiae.
A:Reference number: S33960; MUID:93348778; PMID:8394042
A:Accession: S33962
A:Molecule type: DNA
A:Residues: 1-175 <CHE>
A:Cross-references: GB:X69765; NID:g296985; PIDN:CAA49421.1; PID:g296988
A:Experimental source: strain S288C
R:Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, J.
Submitted to the Protein Sequence Database, March 1994
A:Reference number: S37825
A:Accession: S38022
A:Molecule type: DNA
A:Residues: 1-175 <WIE>
A:Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKUL900A
A:Experimental source: strain S288C
R:Maia e Silva, A.; Bossier, P.; Villela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; J.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38024
A:Accession: S38027

Best Local Similarity 26.1%; Pred. No. 1.4e-08;
Matches 41; Conservative 41; Mismatches 62; Indels 13; Gaps 3;

QY 24 KQIILAHRRFELLPOEQTSSSLRAQVPEQLISLEPLKANPFRICRPFSTSPAK 83
D 20 REVDVLRKRFKMLDKDNGSTTER-----EEFLSLPOLSTNPPLATRIAIFDENGGG 71

QY 84 DLSLEDFDLTLVSFSDFTAPDIKSHYAFRIPDFDDGTLNRKXLSRLVNCITGEGEDTR 143
D 72 D-VDFEYVSGLSAFSRKNGKEKLFARFVYIDRDGYISNGLFVLMKMGV----SN 126

QY 144 LSASEKQILIDNLEESDIDRGTINLSEFOHYSRS 180
D 127 LKDDQLQRIYDKIMEADDKDGKISFEFTKVENT 163

RESULT 5
A33391
calcineurin regulatory chain - human
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
A:Accession: A33391
R:Guerini, D.; Kirilovs, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A:Reference number: A33391; MUID:90126237; PMID:2558868
A:Accession: A33391
A:Molecule type: mRNA
A:Residues: 1-170 <GDE>
A:Cross-references: GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705
C:Genetics:
A:Gene: GDB:PPP3R1; CALNB
A:Cross-references: GDB:136804; OMIM:601302
A:Map position: 2p16-2p15
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status predicted <KAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status predicted
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status predicted

Query Match 19.2%; Score 183.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQLSLPELKNPFRICRPFSTSPAKDSLSEDFDLTLVSFSDFTAPDIKSHYAFRI 115
D 41 EEFMSLPELQNPVQVRVIDITD-D-GNGEYDFKFEIIGVSOFSVKGKREQLRFAFRY 99

QY 116 DFDDGTLNRKXLSRLVNCITGEGEDTRLSASEMKQILIDNLEESDIDRGTINLSEFOH 175
D 100 DMDKDGYSINGLFQVLKMGV-----NNLKDTQIQIYDKITINADKDGGRISFEFCA 155

QY 176 VI 177
D 156 VV 157

RESULT 6
S34127
calcineurin regulatory chain [validated] - bovine
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C:Accession: I45831; J0297; S34127
R:Nargang, C.E.; Bortoff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A:Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A:Reference number: I45831; MUID:95102111; PMID:7803816
A:Accession: I45831
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <NAB>
A:Cross-references: EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969
R:Altken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A:Title: The structure of the B subunit of calcineurin.
A:Reference number: J0297; MUID:84132092; PMID:6321184
A:Accession: J0297
A:Molecule type: protein
A:Residues: 2-11, 13-153, 155-169 <ATD>
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Slutchak, M.D.; Thomson, J.A.; Fitzgibbon, submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66708; PDB:1TCO
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Slutchak, M.D.; Thomson, J.A.; Fitzgibbon, Cell 82, 507-522, 1995
A:Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant
A:Reference number: A56967; MUID:95360994; PMID:7543369
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status experimental <KAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experiment
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experiment
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experiment
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status experiment
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status experiment

Query Match 19.2%; Score 183.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQLSLPELKNPFRICRPFSTSPAKDSLSEDFDLTLVSFSDFTAPDIKSHYAFRI 115
D 41 EEFMSLPELQNPVQVRVIDITD-D-GNGEYDFKFEIIGVSOFSVKGKREQLRFAFRY 99

QY 116 DFDDGTLNRKXLSRLVNCITGEGEDTRLSASEMKQILIDNLEESDIDRGTINLSEFOH 175
D 100 DMDKDGYSINGLFQVLKMGV-----NNLKDTQIQIYDKITINADKDGGRISFEFCA 155

QY 176 VI 177
D 156 VV 157

RESULT 7
JC1220
calcineurin regulatory chain, brain - mouse
N:Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: JC1220
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A:Title: Structure and expression of the murine calmodulin-dependent
A:Reference number: JC1220; MUID:92392379; PMID:1325794
A:Accession: JC1220
A:Molecule type: mRNA
A:Residues: 1-170 <DNR>
A:Cross-references: GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

```

QY   116 DFDDGTLNREXLSRLVNCITGEGEDTRLASASEMKQLIDNLIEESDIDRGTINLSEFQH 175
      |||||::|:::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   146 DMDKDGYSINGELFQVLKMMVG----NNLKDTOLQQIVDKVTIINADKGDRISFEFCA 201
      QY   176 VI 177
      Db   202 VW 203

RESULT 9
T22708
hypothetical protein F55C10.1 - Caenorhabditis elegans
C:Species:Caenorhabditis elegans
C:Date:15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22708
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19603
A:Accession: T22708
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <WIL>
A:Cross-references: EMBL:Z74036; PIDN:CAA98489.1; GSPDB:GN00023; CESP:F55C10.1
A:Experimental source: clone F55C10
C:Genetics:
A:Gene: CESP:F55C10.1
A:Map position: 5
A:Introns: 159/2; 199/3; 213/1; 272/1; 312/3; 353/3

Query Match          18.9%; Score 180.5; DB 2; Length 369;
Best Local Similarity 27.8%; Pred. No. 6.1e-07;
Matches 50; Conservative 37; Mismatches 70; Indels 23; Gaps 6;

QY   3 GSGRSLSKELLAEQ--DLATFLTKQEILLAHRRFCCELLPQQRTVESLSRAQVPPEQILS 60
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   200 GADASLPMECSNFDAVELRLT-----RRFKKL-----DVDS--GSLSVVEEPM 243

QY   61 LPELKANPFKERICRVFTSPAKDSLSDFDLDLLSVFSDTATPDIKSHYAFRIFDFDD 120
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   244 LPELQNPLQVRVIDFD-EDNGNEVDVFREFIQIGISQFSVKGDKNLTKLFAFRIVDMRD 302

QY   121 GTLNREXLSRLVNCITGEGEDTRLASASEMKQLIDNLIEESDIDRGTINLSEFQHVSR 180
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   303 GFISNGELFQVLKMMVG---NNLKDSOLOQIVDKVTILFHDKDGDGKISFQEFCDVWEHT 358

RESULT 10
JC5174
calcineurin regulatory chain 2 - fruit fly (Drosophila melanogaster)
N:Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein
C:Species: Drosophila melanogaster
C:Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
C:Accession: JC5174
R:Warren, W.D.; Phillips, A.M.; Howells, A.J.
Gene 177, 149-153, 1996
A:Title: Drosophila melanogaster contains both x-linked and autosomal homologues
A:Reference number: JC5174; MUID: J7080515; PMID: 8921860
A:Accession: JC5174
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <WAR>
A:Cross-references: GB:U56245; NID:g1336009; PIDN:AAC47350.1; PID:g1336010
C:Comment: This protein is the calcium binding chain of calcineurin, involved
C:Genetics:
A:Gene: dcnB2
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
```

F:128-160/Domain: calmodulin repeat homology <EF4>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 18.3%; Score 175.5; DB 2; Length 170;
 Best Local Similarity 24.7%; Pred. No. 6e-07;
 Matches 44; Conservative 42; Mismatches 73; Indels 19; Gaps 4;
 3 GSGSRSLKELLAEYODTLFTLKOEILAHRRFCELLPQEQRTVSSLRAGVFEQILSLP 62
 Db 2 GNESLPLMEKMSND-----ADELRKGRF-----RKLDLDSGALSVDDEMSLP 47
 Oy 63 ELKANPKEKICRVFSTSPAKDSLFEDFLDLVSFSDTAPDPIKSHYAFRIFFDDGDT 122
 Db 48 ELQONPLVQAVIDIFD-ADNGEYDFKEFIQGVSGFVKDKSLRFAFRFYDDNDGXY 106
 Oy 123 LNRXSLVNLCTGEGEDTRLASSEMKQIDNTEESDIDRDGTINLSEFOHVISRS 180
 Db 107 ISNGELFOVLMKMWG-----NNLKDTOLQOIVDKITGFADKDEGKISDFECVVGNT 160

RESULT 11

JC1242
 calcineurin regulatory subunit, calcineurin B - scallop (Patinopecten yessoensis)
 N:Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory subunit
 C:Species: Patinopecten yessoensis (Yesso scallop)
 C>Date: 09-Jun-2000 #sequence-revision 09-Jun-2000 #text-change 21-Jul-2000
 C:Accession: J07242; PC7070
 R:Oryu, M.; Nakatomi, A.; Watanabe, M.; Hatsuuse, R.; Yazawa, M.
 J. Biochem. 127, 739-746, 2000
 A:Title: Molecular cloning of cDNA encoding two subunits of calcineurin from scallop testis
 A:Reference number: J07241
 A:Accession: J07242

A:Molecule type: mRNA
 A:Residues: 1-170 <UR>
 A:Cross-references: DDBJ:AB041524
 A:Experimental source: testis
 A:Accession: PC7070
 A:Molecule type: protein
 A:Residues: 12-68;73-85;92-170 <UR2>
 C:Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-specific protein to the regulation of flagellar motility.
 C:Genetics:
 A:Gene: cnb
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; flagellar rotation; myristylation; phosphoprotein;

Query Match 18.0%; Score 172.5; DB 2; Length 170;
 Best Local Similarity 25.1%; Pred. No. 1e-06;
 Matches 44; Conservative 40; Mismatches 72; Indels 19; Gaps 4;
 3 GSGSRSLKELLAEYODTLFTLKOEILAHRRFCELLPQEQRTVSSLRAGVFEQILSLP 62
 Db 2 GNESLPLMEKMSND-----PEIKRLGRF-----RKLDLDSGALSVDDEMSLP 47
 Oy 63 ELKANPKEKICRVFSTSPAKDSLFEDFLDLVSFSDTAPDPIKSHYAFRIFFDDGDT 122
 Db 48 ELQONPLVQAVIDIFD-ADNGEYDFKEFIQGVSGFVKDKSLRFAFRFYDDNDGXY 106
 Oy 123 LNRXSLVNLCTGEGEDTRLASSEMKQIDNTEESDIDRDGTINLSEFOHVISRS 177
 Db 107 ISNGELFOVLMKMWG-----NNLKDTOLQOIVDKITGFADKDEGKISDFECVVGNT 157

RESULT 12

A44307
 calcineurin regulatory chain 1 - fruit fly (Drosophila melanogaster)
 N:Alternate names: calcineurin beta subunit; calcineurin chain B-1; phosphoprotein phosphatase
 C:Species: Drosophila melanogaster
 C>Date: 30-Apr-1993 #sequence-revision 18-Nov-1994 #text-change 13-Aug-1999
 C:Accession: A44307
 R:Guerini, D.; Montell, C.; Klee, C.B.
 J. Biol. Chem. 267, 22542-22549, 1992

A:Title: Molecular cloning and characterization of the genes encoding the two subunits of calcineurin
 A:Reference number: A44307; MUID:93054551; PMID:1331060
 A:Accession: A44307

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-170 <GUE>
 A:Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
 A>Note: sequence extracted from NCBI Backbone (NCBIF:117113)
 C:Genetics:
 A:Gene: FlyBase:FBgn0010014
 A:Cross-references: FlyBase:FBgn0010014

C:Complex: heterodimer with calcineurin catalytic chain
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
 F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
 F:18-49/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>
 F:87-119/Domain: calmodulin repeat homology <EF3>
 F:128-160/Domain: calmodulin repeat homology <EF4>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.9%; Score 171.5; DB 2; Length 170;
 Best Local Similarity 26.5%; Pred. No. 1.2e-06;
 Matches 41; Conservative 37; Mismatches 64; Indels 13; Gaps 3;
 26 EILAHRRFCELLPQEQRTVSSLRAGVFEQILSLPELKANPKEKICRVFSTSPAKDS 85
 Db 19 EIRLRGRF-----RKLDLDSGALSVDDEMSLPQONPLVQAVIDIFD-ADNGE 69
 Oy 86 LSFEDFLDLVSFSDTAPDPIKSHYAFRIFFDDGDTLNRXSLVNLCTGEGEDTRL 145
 Db 70 VDFKEFIQGVSGFVKDKSLRFAFRFYDDNDGXYISNGELFOVLMKMWG-----NNLK 125
 Oy 146 ASEMKQIDNTEESDIDRDGTINLSEFOHVISRS 180
 Db 126 DTOLQOIVDKITGFADKDEGKISDFECVVGNT 160

RESULT 13

JC1221
 calcineurin regulatory chain, testis - mouse
 N:Alternate names: calcineurin beta-2 subunit; calcineurin chain B-2; phosphoprotein
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 13-Aug-1999
 C:Accession: J01221

R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
 Biochem. Biophys. Res. Commun. 187, 537-543, 1992
 A:Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase II
 A:Reference number: J01220; MUID:92392379; PMID:1325794
 A:Accession: J01221
 A:Molecule type: mRNA
 A:Residues: 1-179 <UR>
 A:Cross-references: GB:S43865; NID:g255080; PIDN:AA23172.1; PID:g255081
 A:Experimental source: testis
 C:Comment: With calcineurin catalytic chain plays an important role in neural and muscle function

A:Gene: pp2b-beta-2
 C:Complex: heterodimer with calcineurin catalytic chain
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
 F:2-179/Product: calcineurin regulatory chain #status predicted <MAT>
 F:18-49/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>
 F:87-119/Domain: calmodulin repeat homology <EF3>
 F:128-160/Domain: calmodulin repeat homology <EF4>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.7%; Score 169.5; DB 2; Length 179;
 Best Local Similarity 27.8%; Pred. No. 1.9e-06;
 Matches 42; Conservative 29; Mismatches 67; Indels 13; Gaps 3;

QY 35 CELLPQEQ-----RTVESSLRQVFFEQILSLPELKPANPKFRCRVFSTSPAKDSL 86
 Db 12 CNHFDEEIRLGRKSLDKSGSLSEIEFMRLPQLQNPVGRVIDIFDFTD-GNGEV 70
 QY 87 SFEDFLDLVSFSDTATPDIKSHVAFRFDFFDDGTLNREXLSRLVNLCTGEGEDTRL 146
 Db 71 DFHEFIVTQSFVKGDEEQKLRFAFRIYDMNDGFIISNGELFQVLKMMVG-----NNLKD 126
 QY 147 SEMKQLDNLILEESDIDRGTINLSEFQHV 177
 Db 127 WLOQLVDKSLVLDKDGGRISPEEFSDV 157

RESULT 14

PS0261
 calcineurin regulatory chain-like;protein, testis - rat (fragment)
 N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
 C:Accession: PS0261
 R:Sugimoto, M.; Matsui, H.; Etoh, S.; Shimizu, T.; Nishio, H.; Mola, L.J.M.P.; Tokuda, M.
 Biochem. Biophys. Res. Commun. 180, 1476-1482, 1991
 A:Title: Isolation and sequence of rat testis cDNA for a calcium binding polypeptide sim
 A:Reference number: PS0261; MUID:92062183; PMID:1659420
 A:Accession: PS0261
 A:Molecule type: mRNA
 A:Residues: 1-165 <SUG>
 A:Cross-references: GB:S63991; NID:g238643; PIDN:AAB20281.1; PID:g238644
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand
 F:7-38/Domain: calmodulin repeat homology <EF1>
 F:39-71/Domain: calmodulin repeat homology <EF2>
 F:76-108/Domain: calmodulin repeat homology <EF3>
 F:117-149/Domain: calmodulin repeat homology <EF4>

Query Match 17.5%; Score 167.5; DB 2; Length 165;
 Best Local Similarity 31.1%; Pred. No. 2.5e-06;
 Matches 38; Conservative 27; Mismatches 52; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANPKFRCRVFSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHVAFRIF 115
 Db 30 DEFMSLPQLQNPVGRVIDIFDFTD-GNGEVDREFRIVGTQSFVKGDEEQKLRFAFRIY 88
 QY 116 DFDDGTLNREXLSRLVNLCTGEGEDTRLSEMKQLDNLILEESDIDRGTINLSEFQHV 175
 Db 89 DMDNDGFIISNGELFQVLKMMVG-----NNLKDQQLQVLDKSLVLDKDGGRISPEEPRD 144
 QY 176 VI 177
 Db 145 VV 146

RESULT 15

JQ1232
 calcineurin regulatory chain-like protein - rat
 N:Alternate names: calcineurin chain B-like protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
 C:Accession: JQ1232
 R:Mukai, H.; Chang, C.D.; Tanaka, H.; Ito, A.; Kuno, T.; Tanaka, C.
 Biochem. Biophys. Res. Commun. 179, 1325-1330, 1991
 A:Title: cDNA cloning of a novel testis-specific calcineurin B-like protein.
 A:Reference number: JQ1232; MUID:92028870; PMID:1718268
 A:Accession: JQ1232
 A:Molecule type: mRNA
 A:Residues: 1-176 <MUK>
 A:Cross-references: GB:D10393; GB:D90449; NID:g220687; PIDN:BAA01232.1; PID:g220688
 A:Experimental source: testis
 A>Note: this protein appears to be expressed specifically in testis
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; lipoprotein; myris
 F:2-176/Product: calcineurin regulatory chain-like protein #status predicted <MAY>
 F:18-49/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>
 F:87-119/Domain: calmodulin repeat homology <EF3>
 F:128-160/Domain: calmodulin repeat homology <EF4>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.5%; Score 167.5; DB 2; Length 176;
 Best Local Similarity 31.1%; Pred. No. 2.7e-06;
 Matches 38; Conservative 27; Mismatches 52; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANPKFRCRVFSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHVAFRIF 115
 Db 41 DEFMSLPQLQNPVGRVIDIFDFTD-GNGEVDREFRIVGTQSFVKGDEEQKLRFAFRIY 99
 QY 116 DFDDGTLNREXLSRLVNLCTGEGEDTRLSEMKQLDNLILEESDIDRGTINLSEFQHV 175
 Db 100 DMDNDGFIISNGELFQVLKMMVG-----NNLKDQQLQVLDKSLVLDKDGGRISPEEPRD 155
 QY 176 VI 177
 Db 156 VV 157

Search completed: January 17, 2003, 12:43:32
 Job time : 18 secs

Fri Jan 17 13:03:49 2003

mutl127.ra1

Page 1

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 15 Seconds

(without alignments)
374.652 Million cell updates/sec

Title: MUT127

Perfect score: 957
Sequence: 1 MGGSSRLSKELLAEYQDLT.....EPQHYSKSPDRASSFKIYL 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	951	99.4	191	4	US-08-720-625-2
2	945	98.7	191	4	US-08-764-563-1
3	213.5	22.3	177	3	US-08-764-563-3
4	201.5	21.1	174	1	US-08-328-322-17
5	190.5	19.9	157	1	US-08-328-322-15
6	183.5	19.2	169	4	US-08-720-625-4
7	183.5	19.2	170	3	US-08-764-563-5
8	173	18.1	186	3	US-08-655-352-8
9	173	18.1	186	4	US-09-258-016-8
10	173	18.1	186	4	US-09-257-825B-8
11	169.5	17.7	179	3	US-08-764-563-4
12	150.5	15.7	196	3	US-09-048-889-1
13	147	15.4	193	3	US-08-655-352-3
14	147	15.4	193	4	US-09-258-016-3
15	147	15.4	193	4	US-09-257-825B-3
16	140	14.6	220	4	US-09-359-913-26
17	140	14.6	220	4	US-08-298-731-26
18	139	14.5	191	4	US-08-655-352-7
19	139	14.5	191	4	US-09-258-016-7
20	139	14.5	191	4	US-09-257-825B-7
21	136	14.2	193	3	US-08-655-352-2
22	136	14.2	193	4	US-09-258-016-2
23	135	14.1	193	4	US-08-257-825B-2
24	135	14.1	216	4	US-09-399-913-6
25	135	14.1	216	4	US-09-298-731-6
26	135	14.1	220	4	US-09-399-913-24
27	135	14.1	220	4	US-09-298-731-24

28	135	14.1	227	4	US-09-399-913-8	Sequence 8, Appl1
29	135	14.1	227	4	US-09-399-913-10	Sequence 10, Appl1
30	135	14.1	227	4	US-09-298-731-8	Sequence 8, Appl1
31	135	14.1	227	4	US-09-298-731-10	Sequence 10, Appl1
32	135	14.1	245	4	US-09-399-913-4	Sequence 4, Appl1
33	135	14.1	245	4	US-09-398-731-4	Sequence 4, Appl1
34	135	14.1	252	4	US-09-399-913-20	Sequence 20, Appl1
35	135	14.1	252	4	US-09-298-731-20	Sequence 20, Appl1
36	135	14.1	270	4	US-09-399-913-14	Sequence 14, Appl1
37	135	14.1	270	4	US-09-298-731-14	Sequence 14, Appl1
38	134	14.0	216	4	US-09-399-913-2	Sequence 2, Appl1
39	134	14.0	216	4	US-09-298-731-2	Sequence 2, Appl1
40	132	13.8	270	4	US-09-399-913-18	Sequence 18, Appl1
41	132	13.8	270	4	US-09-298-731-18	Sequence 18, Appl1
42	131	13.7	193	3	US-08-655-352-4	Sequence 4, Appl1
43	131	13.7	193	4	US-09-258-016-4	Sequence 4, Appl1
44	131	13.7	193	4	US-09-257-825B-4	Sequence 4, Appl1
45	130	13.6	191	3	US-08-655-352-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Nalk, Ulhas P.
TITLE OF INVENTION: CALCIDIUM-INTRIGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
SMITH: P. O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720.625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2
Query Match 99.4% Score 951; DB 4; Length 191;
Best Local Similarity 99.0% Pred. No. 4.8e-99;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGGSSRLSKELLAEYQDLTFLTKOELLARRPCELLPOBORVYESSLRQVPEQILS 60
DB 1 MGGSSRLSKELLAEYQDLTFLTKOELLARRPCELLPOBORVYESSLRQVPEQILS 60
QY 61 LPELKANFKERICQVFSTSPAKDSLSFEDFLDLSTVSDPATPDIKSHYAFRFDPDD 120

Db 61 LPELKANPKEICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120

QY 121 GTLNREXLSRLVNCJTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180

Db 121 GTLNREXLSRLVNCJTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180

QY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1

; Sequence 1, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08764.563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 191 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: Consensus

; CLONE: Consensus

US-08-764-563-1

Query Match 98.7%; Score 945; DB 3; Length 191;

Best Local Similarity 98.4%; Pred. No. 2.3e-98;

Matches 188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPQEQRTVSSSLRAQVFFEQILS 60

Db 1 MGGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPQEQRTVSSSLRAQVFFEQILS 60

QY 61 LPELKANPKEICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120

Db 61 LPELKANPKEICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120

QY 121 GTLNREXLSRLVNCJTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180

Db 121 GTLNREXLSRLVNCJTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180

QY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 3

US-08-764-563-3

; Sequence 3, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08764.563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 458230

US-08-764-563-3

Query Match 22.3%; Score 213.5; DB 3; Length 177;

Best Local Similarity 29.2%; Pred. No. 2.9e-16;

Matches 52; Conservative 39; Mismatches 74; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLAAHRRFCELLPQEQRTVSSSLRAQVFFEQILS 60

Db 1 MGTNTSLRPEEVEEMQKGTFTQKIKKLYKRFKLDKDGNGTISK-----DEFLM 52

QY 61 LPELKANPKEICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120

Db 53 IPELAYNPLVKRVISIFDEN-GDGSVNFKEFIALSVFNAGQKQKLEFAFKVYDIDGD 111

QY 121 GTLNREXLSRLVNCJTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIS 178

Db 112 GYISNGELFTVLMKMWG----NNLSVDVQLQIIVDKTILEADGDGDKGISPEEFKATLS 165

RESULT 4

US-08-328-322-17

; Sequence 17, Application US/08328322

```

; Patent No. 5723436
; GENERAL INFORMATION:
; APPLICANT: Huang, Laiqiang
; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-322-17

Query Match 21.1%; Score 201.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 6.3e-15;
Matches 48; Conservative 43; Mismatches 69; Indels 17; Gaps 4;

OY 1 MGGSGRLSKELLAEYQDITFLTKOELLAHRRFCLPQEQRTVSSSLRAQVPEFOIIS 60
DB 1 MGAAPSKIVDGLLED---TNFDRDEIERLRKRFMKLIDSSGSGIDKN-----EFMS 48
OY 61 LPELKNPFKERICRVFSTSPAKDSLSEFDFDLDSFSDTAPDIXSHYAFRIEPPDD 120
DB 49 IPGVSSNPLAGRIMEVFDADNSGD-VDFQEFITGLSIFSGRSGKDEKLRFAFIYDIDKD 107
OY 121 GTLNEXLSRLVNCLTGEGEDTRLSASEMKQIDNILESDIDRDGTINLSEFOHYI 177
DB 108 GFISNGELFIVLKIWVG-----SNLDEQLOQIVDRITVENSDSGDGRSLSEFEERKNI 160

RESULT 5
; US-08-328-322-15
; Sequence 15, Application US/08328322
; Patent No. 5723436
; GENERAL INFORMATION:
; APPLICANT: Huang, Laiqiang
; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-322-15

Query Match 19.9%; Score 190.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 9.3e-14;
Matches 42; Conservative 39; Mismatches 60; Indels 13; Gaps 3;

OY 24 KOELLAHRRFCELLPQEQRTVSSSLRAQVPEFOIISLPELKNPFKERICRVFSTSPAK 83
DB 3 RDEIERLRKRFMKLIDRSSGSGIDKN-----EFMSIPGVSSNPLAGRIMEVFDADNSG 54
OY 84 DLSFEFDFDLDSFSDTAPDIXSHYAFRIEPPDDGTINRKLXSLVNCLTGEGEDTR 143
DB 55 D-VDFQEFITGLSIFSGRSGKDEKLRFAFIYDIDRDGTINLSEFOHYI 109
OY 144 LSASEMKQIDNILESDIDRDGTINLSEFOHYI 177
DB 110 LDDEQLOQIVDRITVENSDSGDGRSLSEFEERKNI 143

RESULT 6
; US-08-720-625-4
; Sequence 4, Application US/08720625
; Patent No. 6242587
; GENERAL INFORMATION:
; APPLICANT: Naik, Ulhas P.
; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6242587th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,625
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 3470-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-720-625-4

Query Match 19.2%; Score 183.5; DB 4; Length 169;
Best Local Similarity 31.1%; Pred. No. 6.4e-13;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQILSPKLPKANKPFRICRVFSTSPAKDSLSFDFDLVSVSTATPDIKSHYAFRIF 115
DB 40 EEFMSLPQLQNPVQRVIDIFDTD-GNGEVDKFEFIEGVSVKQKQKLRFAFRIF 98
QY 116 DFDDGTINREXLSRLVNLCTGEGEDTRLSASEMKQLDNLILEESDIDRDCGTINLSEFOH 175
DB 99 DMDKDGYSNGELFQVLKMMVG-NNLKDTQLQOIIVDKTIINADKDGGRISFEFCA 154
QY 176 VI 177
DB 155 VV 156

RESULT 7
US-08-764-563-5
Sequence 5, Application US/08764563
Patent No. 6093565
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,563
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0178 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 461682
US-08-764-563-5

Query Match 19.2%; Score 183.5; DB 3; Length 170;

Best Local Similarity 31.1%; Pred. No. 6.4e-13;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;
QY 56 EQILSPKLPKANKPFRICRVFSTSPAKDSLSFDFDLVSVSTATPDIKSHYAFRIF 115
DB 41 EEFMSLPQLQNPVQRVIDIFDTD-GNGEVDKFEFIEGVSVKQKQKLRFAFRIF 99
QY 116 DFDDGTINREXLSRLVNLCTGEGEDTRLSASEMKQLDNLILEESDIDRDCGTINLSEFOH 175
DB 100 DMDKDGYSNGELFQVLKMMVG-NNLKDTQLQOIIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 8
US-08-655-352-8
Sequence 8, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovaiiah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
CITY: Suite 1600
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequenin
DESCRIPTION: (Gen2:Drofreq) with homology to lily
DESCRIPTION: CCAMK
US-08-655-352-8

Query Match 18.1%; Score 173; DB 3; Length 186;
Best Local Similarity 25.4%; Pred. No. 1.1e-11;
Matches 50; Conservative 39; Mismatches 86; Indels 22; Gaps 5;
QY 1 MGGSGSRLSKELIAEYQDLTTLTKQKILLAHRRFCCLLPQEQRTVSSLRQVPPFEILS 60
DB 1 MGKSKSLKQDITDLTTLTKQKILLAHRRFCCLLPQEQRTVSSLRQVPPFEILS 60

QY 61 LPELKANPKEKICRVFSTSPAKDSLSFEDFLDLLSVFSDTAPDINKSHAFRIEDDD 120
 Db 56 FPGODPSKFSALVFRVFDEN-NDGSIFFEEFIRALSVTSKGL--DEKLOMAFRILYDVND 112
 QY 121 GTLNREXLSRLVNCU-----TGEGEDTRLSASEKOLIDNILEESDIDRGDTINLSE 172
 Db 113 GYITREEMNIVDAIYQWGOQPOSEDENT-----PQKRVDKIFDQMKNDKNDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 9
 US-09-258-016-8
 ; Sequence 8, Application US/09258016
 ; Patent No. 6362395
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachettira W. Poovaiyah, Zhilua Liu,
 ; APPLICANT: Shameekumar Patil, Dalsuke Takekawa
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ; ADDRESSEE: Whinston, LLP
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/258, 016
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephens Jr., Donald L.
 ; REGISTRATION NUMBER: 34,022
 ; REFERENCE/DOCKET NUMBER: 4630-51994
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 186 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: Region of Drosophila frequenta
 ; DESCRIPTION: (Gen2:Id:Protein) with homology to 111y
 ; DESCRIPTION: CCMK
 ; US-09-258-016-8

Query Match 18.1%; Score 173; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 1.1e-11;
 Matches 50; Conservative 39; Mismatches 86; Indels 22; Gaps 5;

QY 1 MGSGSRLSKELLAEYODTLFLTKOELLAHRRFCCELLPOEQRIVESSLRQAQVEEQILS 60
 Db 1 MGKSSSKLKODITDLITDTYFEKEIKRQWKGFLKDCPNGLTGOGFIKIKYKPF----- 55
 QY 61 LPELKANPKEKICRVFSTSPAKDSLSFEDFLDLLSVFSDTAPDINKSHAFRIEDDD 120
 Db 56 FPGODPSKFSALVFRVFDEN-NDGSIFFEEFIRALSVTSKGL--DEKLOMAFRILYDVND 112

QY 121 GTLNREXLSRLVNCU-----TGEGEDTRLSASEKOLIDNILEESDIDRGDTINLSE 172
 Db 113 GYITREEMNIVDAIYQWGOQPOSEDENT-----PQKRVDKIFDQMKNDKNDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 10
 US-09-257-825B-8
 ; Sequence 8, Application US/09257825B
 ; Patent No. 6403352
 ; GENERAL INFORMATION:
 ; APPLICANT: Poovaiyah, Bachettira W.
 ; APPLICANT: Patil, Shameekumar
 ; APPLICANT: Takekawa, Dalsuke
 ; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plai
 ; FILE REFERENCE: 4630-51993
 ; CURRENT APPLICATION NUMBER: US/09/257, 825B
 ; CURRENT FILING DATE: 1999-02-25
 ; PRIOR APPLICATION NUMBER: US 08/655,352
 ; PRIOR FILING DATE: 1996-05-23
 ; PRIOR APPLICATION NUMBER: US 60/014,743
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 ; US-09-257-825B-8

Query Match 18.1%; Score 173; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 1.1e-11;
 Matches 50; Conservative 39; Mismatches 86; Indels 22; Gaps 5;

QY 1 MGSGSRLSKELLAEYODTLFLTKOELLAHRRFCCELLPOEQRIVESSLRQAQVEEQILS 60
 Db 1 MGKSSSKLKODITDLITDTYFEKEIKRQWKGFLKDCPNGLTGOGFIKIKYKPF----- 55
 QY 61 LPELKANPKEKICRVFSTSPAKDSLSFEDFLDLLSVFSDTAPDINKSHAFRIEDDD 120
 Db 56 FPGODPSKFSALVFRVFDEN-NDGSIFFEEFIRALSVTSKGL--DEKLOMAFRILYDVND 112
 QY 121 GTLNREXLSRLVNCU-----TGEGEDTRLSASEKOLIDNILEESDIDRGDTINLSE 172
 Db 113 GYITREEMNIVDAIYQWGOQPOSEDENT-----PQKRVDKIFDQMKNDKNDKLTLEE 166
 QY 173 FOHVISRSPDFASSFKI 189
 Db 167 FREGSKADPRIVQALSL 183

RESULT 11
 US-08-764-563-4
 ; Sequence 4, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goll, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

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;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/764,563
;; FILING DATE: Herewith
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0178 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 179 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 109612
US-08-764-563-4

Query Match 17.7%; Score 169.5; DB 3; Length 179;
Best Local Similarity 27.8%; Pred. No. 2.6e-11;
Matches 42; Conservative 29; Mismatches 67; Indels 13; Gaps 3;

QY 35 CELLPQEQ-----RTVESLRAQVFEQILSLPELKANPFRICRVSTSPAKDSL 86
Db 12 CNHFQDEIRRLGKFRKLDLKSGLSIEEFMRPLPQNPVGRVIDFTD-GNGEV 70
QY 87 STEFDLLSVSDATPDIKSHYAFRFDGDTLNREXLSRLVNCLTGEGEDTRLSA 146
Db 71 DFHEFIVTGSQFVKGEQKLRFAFYDMNDGFIISNGELFQVLRKMVG-----NNLKD 126
QY 147 SEMKOLIDNILEESDIDRGTINLSEFQHV 177
Db 127 WOLQQLVDRKSLVLDKDGGRISFEFSDV 157

RESULT 12
US-09-048-889-1
; Sequence 1, Application US/09048889
; Patent No. 6117989
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lal, Preeti
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,889
; FILING DATE: Herewith
```

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;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cerrone, Michael C.
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0493 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 196 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: COLNNOT09
;; CLONE: 1846517
US-09-048-889-1

Query Match 15.7%; Score 150.5; DB 3; Length 196;
Best Local Similarity 23.3%; Pred. No. 4e-09;
Matches 44; Conservative 38; Mismatches 74; Indels 33; Gaps 6;

QY 5 GSRLSKELLAQYQDL---TELTKOEILLAHRRFCCLLPQEQRTVESLRAQVPEQILS 60
Db 2 GSRTSHAIVPDGSIIRRETGFSQASLRLHHRF-----RALDRNKKGVLSRMDLQQ 53
QY 61 LPELKANPFRICRVSTSPAKDSLSPEDFLDLLSVF-----SDTATPDIKS----- 108
Db 54 IGAVALNPGLRIETSEFPFG-GSQRVDFGFRVLAHFRPVEDEDETQDPKKPEPLNSR 112
QY 109 ----HYAFRIFDDDDGTNLNREXLSRLVNCLTGEGEDTRLSASEMKOLIDNILEESDIDR 164
Db 113 RNKLHYAFQYLDLDRDGKISRHEMLQVLRMVG-----VQVTEOLENIADRTVQEADEG 168
QY 165 DGTINLSEF 173
Db 169 DGAVSFVEF 177

RESULT 13
US-08-655-352-3
; Sequence 3, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; CLASSIFICATION: 800
```

```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/323,449
? FILING DATE: October 14, 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Dow, Alan. E.
? REGISTRATION NUMBER: 35,123
? REFERENCE/DOCKET NUMBER: 4630-45000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (503) 226-7391
? TELEFAX: (503) 228-9446
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 193 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? DESCRIPTION: Region of rat neural visinin-like protein
? DESCRIPTION: (Gen2:ratnvp3) with homology to 11ly
? DESCRIPTION: CCAAMK
US-08-655-352-3

```

```

?      REGISTRATION NUMBER: 34,022
?      REFERENCE/DOCKET NUMBER: 4650-51994
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (503) 226-7391
?      TELEFAX: (503) 228-9446
?      INFORMATION FOR SEQ ID NO: 3:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 193 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      DESCRIPTION: Region of rat neural vistin-like protein
?      DESCRIPTION: (Gen2:Ratnvp3) with homology to Illy
?      DESCRIPTION: CCAMK
?
US-09-258-016-3

```

QY 119 DGTNREXLSRLVNCJTGEGETFLSASEMK-----OLIDNILEESDIDRDGTIN 169
Db 112 GNGYISRSEMLEIVQAI-----YMWSSVMKPEDESTPEKRTDKIFQMDINNDGKLS 165
QY 170 LSEF-----OHVISRSPDFASSF 187
Db 166 LEEFIKAKSDPSIVRLLQCDPSSASQF 193

Search completed: January 17, 2003, 12:43:53
Job time : 16 secs

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: January 17, 2003, 12:46:59 : Search time 31 Seconds
(without alignments)
1269.516 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGGSSRLSKELLAEYODLT.....EQHVISRSPDFASSKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_protent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	408	42.6	311	5	Q93640
2	364	38.0	185	11	Q9D9N5
3	341	35.6	187	4	Q96077
4	338.5	35.4	206	5	Q9W205
5	272	28.4	54	6	Q8GL2
6	226.5	23.7	180	5	Q9GP83
7	201	21.0	175	5	Q9U0X7
8	189	19.7	175	10	Q9LS47
9	188	19.6	175	10	Q93VF2
10	183.5	19.2	169	5	Q9NEM1
11	182.5	19.1	244	5	Q20804
12	181.5	19.0	189	5	Q9VNF9
13	179.5	18.8	170	5	Q9NKM7
14	179.5	18.8	170	5	Q9SP81
15	178	18.6	200	5	Q8SRP8
16	176.5	18.4	115	11	Q99L09

17	175.5	18.3	167	5	Q9VWX8	Q9VWX8 drosophila
18	170.5	17.8	175	3	Q9HDE1	Q9HDE1 cryptococcus
19	170.5	17.8	177	3	Q9HDD3	Q9HDD3 cryptococcus
20	170	17.8	274	10	Q9AMW4	Q9AMW4 oryza sativ
21	169.5	17.7	195	5	Q23643	Q23643 caenorhabd1
22	169.5	17.7	213	5	Q16343	Q16343 caenorhabd1
23	169.5	17.7	213	5	Q9LVB8	Q9LVB8 arabidopsis
24	169	17.7	170	4	Q8WYJ4	Q8WYJ4 homo sapien
25	169	17.7	173	4	Q96LZ3	Q96LZ3 homo sapien
26	169	17.7	190	5	Q9NAY9	Q9NAY9 naegleria f
27	164.5	17.2	161	10	Q9AY39	Q9AY39 oryza sativ
28	163.5	17.1	226	10	Q81446	Q81446 arabidopsis
29	158	16.5	130	3	Q96X50	Q96X50 magnaporthe
30	158	16.5	190	3	Q8TGC0	Q8TGC0 magnaporthe
31	153	16.0	196	5	Q9N2Y1	Q9N2Y1 caenorhabd1
32	153	16.0	225	10	Q8W5C8	Q8W5C8 oryza sativ
33	151.5	15.8	226	10	Q81447	Q81447 arabidopsis
34	150.5	15.7	213	10	Q81445	Q81445 arabidopsis
35	150	15.7	246	10	Q82641	Q82641 arabidopsis
36	147	15.4	192	10	Q81328	Q81328 arabidopsis
37	147	15.4	222	10	Q81223	Q81223 arabidopsis
38	145	15.2	191	4	Q9UM19	Q9UM19 homo sapien
39	141.5	14.8	153	5	Q9U5J0	Q9U5J0 trichomonas
40	141.5	14.8	160	5	Q9U5I9	Q9U5I9 trichomonas
41	140	14.6	29	11	Q9UJY5	Q9UJY5 mus musculu
42	137	14.3	216	11	Q9UJ57	Q9UJ57 mus musculu
43	137	14.3	220	4	Q9NS60	Q9NS60 homo sapien
44	137	14.3	220	4	Q9HD11	Q9HD11 homo sapien
45	137	14.3	220	11	Q9JM60	Q9JM60 rattus norv

ALIGNMENTS

RESULT 1

Q93640 PRELIMINARY; PRT; 311 AA.

AC Q93640; 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F30A10.1 protein.
GN F30A10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;

RN (1)
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCR-1996) to the EMBL/Genbank/DBJ databases.

RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;

RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 283:2012-2018(1998).
DR EMBL; Z81072; CAB03019.1; -.
DR HSSP; Q99628; IDGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; EF-hand; 3.
DR Prodom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh. 2.
SQ SEQUENCE 311 AA; 33960 MW; 97AFDAF56A6F526F CRC64;

Query Match 42.6%; Score 408; DB 5; Length 311;
Best Local Similarity 42.0%; Pred. No. 1.2e-27;
Matches 87; Conservative 42; Mismatches 52; Indels 26; Gaps 5;

OY 1 MGGSSRLS-----KELIAEYODLTFLIKOELLAAHRCFELLPQEOFTVSS 48
DB 111 MGNASSLSLELNFSGKGVTFREQDEYODCTFFFRKDIIRLYKRFVYALNPHK---VPTN 167

[illegible]

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RC STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandal D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Broksstein P., Brottier P.,
RA Chertis K.C., Busam D.A., Butler C., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke H., Davidson L.B., Davies A.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downe M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durlin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajuli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AF003452; AAF4635.1; -
DR HSSP: Q99828; IDGV.
DR FLYBase: FBgn0034558; CG9236.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; Efh; 3.
DR PROSITE: PS00018; EF-HAND; 2.
KW Calcium-binding.
SQ
SEQUENCE 206 AA; 23591 MW; B3105F7F70F475A9 CRC64;

Query Match 35.4%; Score 338.5; DB 5; Length 206;
Best Local Similarity 43.8%; Pred. No. 8.2e-22;
Matches 77; Conservative 31; Mismatches 51; Indels 17; Gaps 5;

QY 17 QDLFTLKQELLARHRCCELLPQ--EQRTVESLRQVPEEQILSPETKANPFKERRI 73
DB 43 KDCFFFRKELRHKFRRLRPLVRPMTEGQASVYKVCCEIEKPELR----- 94
QY 74 CRVFSTSPARDSLFEEDFLDLVSFTATPDIKSHYAFRFFDDDDGTLREXLSRLYN 133
DB 95 -EAFNSRD-GGGNSFEEDFLDLVSFSQAPRDIVFAFKITVDQDGFICHAD---LWS 149
QY 134 CINGEGEDTILASSEMQLDNIIEESDIDRGTINLSEFOHVISRSPFASSEFKI 189
DB 150 CLTTMTKN-ELSPHQIADKVEADVDGDKLSTLEFHFVILRAPDFLSTHI 204

RESULT 5
Q9GLJ2 PRELIMINARY; PRT; 54 AA.
AC Q9GLJ2;
DT 01-MAR-2001 (Tremblrel. 16, Created)

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DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267715; AAG25931.1; -
DR HSSP: Q99828; IDGV.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 1.
DR ProDom: PD000012; EF-hand; 1.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 54
FT NON_TER 54
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE8A570A4 CRC64;

Query Match 28.4%; Score 272; DB 6; Length 54;
Best Local Similarity 96.3%; Pred. No. 8.9e-17;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 102 APFDIKSHAFRRFDDDDGTLNRELRLSYNCLTEGEGDTRISASEMKQLDIN 155
DB 1 APFDIKSHAFRRFDDDDGTLNREDLSQLVNCLTEGEGDTRISASEMKQLDIN 54

RESULT 6
Q9GP83 PRELIMINARY; PRT; 180 AA.
AC Q9GP83;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Calcinurin B.
CN CnBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Alchem A.;
RA Alchem A.;
RA Theiss (2000), Department of Fachbereich Biologie,
RA Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RA Alchem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ301668; CAC30026.2; -
DR HSSP: P06705; IAVI.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; Efh; 4.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947EBD280DB6 CRC64;

Query Match 23.7%; Score 226.5; DB 5; Length 180;
Best Local Similarity 29.8%; Pred. No. 3.9e-12;
Matches 53; Conservative 44; Mismatches 66; Indels 15; Gaps 4;

QY 1 MGGSGSRSLKELLAEOYDLFTLKQELLARHRCCELLPQEQRTVESLRQVPEEQILS 60

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Db 1 MGNQHSLLNKEQLEQOMKDNDSFSAELKKLYRRFQMLDKDGGSLTT-----DFELS 52
QY 61 LPELKANPKERICRVFTSPAKDS--LSFEDFLDLSVFSDTATPDIKSHYAFRIFFDD 119
Db 53 IPDLALNLLERVQIQFDON--KNETEFSEFVGTATLSHKGTKEKDLKFLFYIDIC 110
QY 120 DGTNLNREXLSRLVNCLTAGEGDTRLSASEMKQLIDNLEESDIDRGTINLSEFQHV 177
Db 111 DGFISNGELFQVLKMWG---TNLNDVLOQIIVDKTIIEGDKDGKISPDEFIRMI 164
; RESULT 7
Q9U0X7
ID Q9U0X7 PRELIMINARY; PRT; 175 AA.
AC Q9U0X7
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcineurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Tosato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,
RA Rajandream M.A., Barrell B.G.
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL133435; CAB62809.1; -.
DR HSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR PRODOM; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 2.
SQ SEQUENCE 175 AA; 19660 MW; 9448F127F4DFA0EB CRC64;

Query Match 21.0%; Score 201; DB 5; Length 175;
Best Local Similarity 25.3%; Pred. No. 6.3e-10;
Matches 46; Conservative 45; Mismatches 77; Indels 14; Gaps 4;

QY 8 LSKELLAEQDITFTLTKQILLAHRRFCCLLPQEQRTVESSLRAQVPPQIILSPELKAN 67
Db 6 LTAELQNIRESTALTDAQVQLYKFSKL-----NKKSGKITRAEFNSIFALASN 57
QY 68 PKERICRVFTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFDDGDTNLNREX 127
Db 58 PLVDRVLAVMDTD-GDSTVDGDFRALAVLSSATSKEDKLFRTFKMYDVGDDGRISNKD 116
QY 128 LSLVNCVLTAGEGDTRLSASEMKQLIDNLEESDIDRGTINLSEFQHVIRSPFASFF 187
Db 117 LFQMLSIWVG---VNLSQLQIIVDKTIIEADVDKDGITFEFQ-ALAVNSDFGRL 171
QY 188 KI 189
Db 172 NL 173

RESULT 8
Q9LS47
ID Q9LS47 PRELIMINARY; PRT; 175 AA.
AC Q9LS47

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like
DE protein (Hypothetical 20.0 kDa protein).
GN A73G18430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kaniya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At3g18430 (GI:15229640).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026658; BAB01109.1; -.
DR EMBL; AY063789; AAL36096.1; -.
DR EMBL; AY091287; AAM14226.1; -.
DR HSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR PRODOM; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 19.7%; Score 189; DB 10; Length 175;
Best Local Similarity 26.6%; Pred. No. 7e-09;
Matches 49; Conservative 46; Mismatches 65; Indels 24; Gaps 5;

QY 1 MGGSGSRSLSKELLAQYQ---DLTFLTKQIILLAHRRFCCLLPQEQRTVESSLRAQVPE 56
Db 1 MGTSSMLTYDIEEVQSHCHDL--FEQEILSLYQFCQL-----DRNAKGRISAD 50
QY 57 QILSLPELKANPKERICRVFTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFFD 116
Db 51 EFLSVPEFAMNPLSQRLKMW-----DGLNPKDFVAFLSAFSAKASAKROKVLKRYVD 104
QY 117 FDDGTNLNREXLSRLVNCVLTAGEGDTRLSASEMKQLIDNLEESDIDRGTINLSEFQHV 176

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Db 105 SCNGVSKDIMEVLRLDLSG----SFMSDEQREYVLSQLKESGYTSPFLTEDEFIKI 160
QY 177 ISRS 180
Db 161 FGSS 164

RESULT 9
Q93VF2 PRELIMINARY; PRT; 175 AA.
ID Q93VF2
AC Q93VF2
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcineurin-like protein.
GN ECGBL1 OR ECGBL1
OS Eucalyptus camaldulensis (Murray red gum), and
OS Eucalyptus grandis.
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids. II: Myrtales; Myrtaceae; Eucalyptus.
OX NCBI_Taxid=34316, 71139;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;
RA Fairbairn D.J., Gomez-gallego S., Savbridge T., Teasdale R.D.;
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF197334; AAL25650.1;
DR EMBL; AF197330; AAL25647.1;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 2.
DR Prodom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 175 AA; 1997 MW; CAE773EE42A3EF16 CRC64;

Query Match
Best Local Similarity 19.6%; Score 188; DB 10; Length 175;
Matches 47; Conservative 46; Mismatches 69; Indels 20; Gaps 4;

QY 1 MGSGRSLKELAEYOD--LTFLLKOEILAHRRFCELLPOEQRVSSSLRAQVPEQI 58
Db 1 MGNASSMLTYDIEVDHCHNNLPSQDELTVLYERFQL-----DRNAKGFISADEF 52
QY 59 LSLPELKANPFRKRICRVFSTSPAKDSLSEFDLILSVFSDTATPDIKSHYAFRIFFD 118
Db 53 LSYVEFAMNPLSORLKRNV-----DGLNFKDFVAFILSAFSAKSKQKIKELIFRVYSD 106
QY 119 DDGTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILESDDIDROGTINLSEFOHVIS 178
Db 107 CNGKVSNDLILEVLRDLSG----PFMSDEQREYVLSQLKESGYTSPFLTEDEFIKI 162
QY 179 RS 180
Db 163 NS 164

RESULT 10
Q9NFNI PRELIMINARY; PRT; 169 AA.
ID Q9NFNI
AC Q9NFNI
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcineurin B.
GN Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20520966; PubMed=11071287;
RA Mecozzi B., Rossi A., Lazaretti P., Kady M., Kaiser S., Valle C.,

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RA Cioji D., Klinkert M.O.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT Immunolocalization to the excretory system";
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1;
DR HSSP; P06705; ITCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR Prodom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 169 AA; 1913 MW; 878E01D08BC5DC1D CRC64;

Query Match
Best Local Similarity 19.2%; Score 183.5; DB 5; Length 169;
Matches 37; Conservative 32; Mismatches 49; Indels 5; Gaps 2;

QY 56 EDLSLPELKANPFRKRICRVFSTSPAKDSLSEFDLILSVFSDTATPDIKSHYAFRIFF 115
Db 40 KEFMSLPELQNPVLRVRIEFTD-GNCEVDFKEKINMSQPSAKGEKALKFAFKLY 98
QY 116 DPDDGTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILESDDIDROGTINLSEFOH 175
Db 99 DMDKDGYSINGELFVYLKMAVG-----NNLKDTQLQIVDKTIMPDKEDGRISPEEFC 154
QY 176 VIS 178
Db 155 VVS 157

RESULT 11
Q20804 PRELIMINARY; PRT; 244 AA.
ID Q20804
AC Q20804
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE F55C10.1 protein.
GN F55C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dodson R.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT Investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL; Z74036; CAA98489.2;
DR HSSP; P06705; ITCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR Prodom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;

Query Match
Best Local Similarity 19.1%; Score 182.5; DB 5; Length 244;
Matches 50; Conservative 38; Mismatches 69; Indels 23; Gaps 6;

QY 3 GSGSRSLKELAEYO--DLFLLKOEILAHRRFCELLPOEQRVSSSLRAQVPEQI 60

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Db 75 GADASLPNEMCSNDAVELRLRT-----RRFKL-----DVDS--GSLSVBEFMS 118
 Qy 61 LPELKANPFRERICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIFFDD 120
 Db 119 LPELQNPVORVIDFD-EDGNGEVDFREFIQGISQVKGDKNTKLKFAFIYDMDRD 177
 Qy 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQIDNILEESDIDBDGTINLSERQHVSR 180
 Db 178 GFISNGELFQVLKMMVG-----NNLKSQLQOIVDKTLFHKDGDGDKISQFECDCVVEHT 233

RESULT 12
 Q9VNF9 PRELIMINARY; PRT; 189 AA.
 AC Q9VNF9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CG2185 protein (LD19356p).
 GN CG2185.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mundall C.J.,

RA Nunoo J., Pacieb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnik S.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003602; AAF51977.1; -;
 DR EMBL; AY069465; AAL39610.1; -;
 DR HSSP; P06705; IAU1.
 DR FlyBase; FBgn0037358; CG2185.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 1.
 KW Calcium-binding.
 SQ SEQUENCE 189 AA; 21996 MW; 3621BAF72BED845D CRC64;
 Query Match 19.0%; Score 181.5; DB 5; Length 189;
 Best Local Similarity 25.4%; Pred. No. 3.5e-08;
 Matches 48; Conservative 42; Mismatches 78; Indels 21; Gaps 4;
 Qy 1 MGSGSR-LSKELLAAYQDLTLTKQETLLAHRRCCELLPQORTVESSLRAQVPEOIL 59
 Db 1 MGKSSSLFRNEETAQIQEETFPNQIERLYSRFTSLDRNDCGTLR-----EDLM 52
 Qy 60 SLPELKANPFRERICRVSTSPAKDSLSFEDFLDLSV-----SDTATPDIKSHYA 111
 Db 53 RIPELAINPLCERIVHSEFFAESNDRVNFQFMVLAHFRPLRDNKSLNSREELKFA 112
 Qy 112 FRIFDFFDDGTLNREXLSRLVNCLTGEGEDTRLSASEMKQIDNILEESDIDBDGTINLS 171
 Db 113 FKMYDLDDGTVISRDILLSILHMMVG----ANISQDLVSTAERTILEADLCCCGKISFE 168
 Qy 172 EFQHVSR 180.
 Db 169 DFCKALDRT 177
 RESULT 13
 Q9NKKW7 PRELIMINARY; PRT; 170 AA.
 AC Q9NKKW7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Calcineurin B.
 OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidea; Pectinidae; Mizuhopecten.
 OX NCBI_TaxID=6573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;
 RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from
 RT Scallop Testis: Demonstration of Stage-Specific Expression during
 RT Maturation of the Testis."
 RL J. Biochem. 0:0-0(2000).
 DR EMBL; AB041524; BAA94543.1; -;
 DR HSSP; P06705; IAU1.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
 SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;
 Query Match 18.8%; Score 179.5; DB 5; Length 170;
 Best Local Similarity 25.1%; Pred. No. 4.6e-08;
 Matches 44; Conservative 42; Mismatches 70; Indels 19; Gaps 4;
 Qy 3 GSGSRLSKELLAAYQDLTLTKQETLLAHRRCCELLPQORTVESSLRAQVPEOILSLP 62
 Db 3 GSGSRLSKELLAAYQDLTLTKQETLLAHRRCCELLPQORTVESSLRAQVPEOILSLP 62

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:46:44 ; Search time 36 Seconds

(without alignments)
706.969 Million cell updates/sec

Title: MUT127

Perfect score: 957
Sequence: 1 MGSGSRSLKELAEYDLT.....EFQHYNSPPDFASSEFKVL 191

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	953	99.6	191	AAW51215	Amino acid sequenc
2	945	98.7	191	AAW64199	Human interferon r
3	928	97.0	191	AAW62287	Human protein phos
4	374	39.1	172	AAU87324	Human central nerv
5	374	39.1	184	AAW43562	Human polypeptide
6	372	38.9	185	AAW64418	Amino acid sequenc
7	348	36.4	173	AAW64054	Human testicular a
8	348	36.4	173	AAU87612	Human central nerv
9	348	36.4	173	AAW5362	Human reproductive
10	348	36.4	173	AAW43637	Human polypeptide

11	348	36.4	173	22	AAU19952
12	340	35.5	187	22	AAE09736
13	338.5	35.4	206	22	ABW64325
14	239.5	25.0	169	23	ABW41194
15	217	22.7	120	20	AAU11876
16	203.5	21.3	175	20	AAV00881
17	190	19.9	175	21	AAW21178
18	190	19.9	210	21	AAW21177
19	189	19.7	175	21	AAW51856
20	189	19.7	175	23	ABW92557
21	187	19.5	175	21	AAW07824
22	185.5	19.4	170	19	AAW64200
23	185.5	19.4	170	21	AAW09978
24	181.5	19.0	189	22	ABW58936
25	180	18.8	169	21	AAW51587
26	178	18.6	169	21	AAW07825
27	176	18.4	169	21	AAW07825
28	175.5	18.3	187	22	ABW61857
29	175.5	18.3	187	22	ABW67063
30	174.5	18.2	162	22	ABW65554
31	173.5	18.1	170	22	ABW60493
32	169	17.7	170	21	AAW09977
33	169	17.7	170	22	AAO14411
34	169	17.7	173	22	AAW64410
35	169	17.7	187	22	AAU87327
36	169	17.7	189	22	ABW95936
37	169	17.7	189	22	AAU87615
38	169	17.7	189	22	AAW95239
39	169	17.7	189	22	AAW43634
40	169	17.7	189	22	AAW43639
41	169	17.7	189	22	AAU19951
42	163.5	17.1	226	21	AAW47032
43	162.5	17.0	226	21	AAW21763
44	156	16.3	190	21	AAW69996
45	155	16.2	194	22	AAU87585

ALIGNMENTS

RESULT 1
ID AAW51215 standard; Protein: 191 AA.

AC AAW51215;

DT 21-AUG-1998 (first entry)

DE Amino acid sequence of the calcium-integrin binding protein.

KW Human calcium-integrin binding protein; CIB; Integrin alpha IIB;
KW cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;
KW inhibition; blood coagulation; vascular disorder.

OS Homo sapiens.

FT Key Location/Qualifiers
FT Region 116..128
FT /note="EF-hand motif"

FT Region 160..173
FT /note="EF-hand motif"

PN W09814471-A1.

PD 09-APR-1998.

PF 24-SEP-1997; 97MO-US16828.

PR 02-OCT-1996; 96US-0720625.

PA (UNNC-) UNIV NORTH CAROLINA.

PI Naik UP, Parise LV;

Novel human calcu
Human kinase inter
Drosophila melanog
Human ovarian anti
Human 5' EST seque
Calcineurin regula
Zea mays protein f
Arabidopsis thalia
Herbicideally activ
Arabidopsis thalia
Human calcineurin.
Human HCNB protein
Drosophila melanog
Arabidopsis thalia
Zea mays protein f
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human CNBII protei
Calcineurin B subu
Amino acid sequenc
Novel central nerv
Human testicular a
Novel central nerv
Human reproductive
Human polypeptide
Novel human calcu
Arabidopsis thalia
Human receptor-ass
Novel central nerv

XX MO9826056-A1.
 PN 18-JUN-1998.
 XX 25-NOV-1997; 97WO-US21603.
 XX 12-DEC-1996; 96US-0764563.
 XX (INCY-) INCYTE PHARM INC.
 PA Goll SR, Hillman JL;
 XX WPI: 1998-348518/30.
 DR N-PSDB; V398009.
 XX
 PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
 PT prevention and treatment of immuno-suppression, neuro-degeneration,
 PT inflammation and cancer
 XX
 PS Claim 1; Fig 1; 65pp; English.
 XX
 CC The present sequence is a pure human protein phosphatase regulatory
 CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
 CC HCNB, are used to produce recombinant HCNB which is used to treat or
 CC prevent immunosuppression or neurological diseases (especially parasitic,
 CC bacterial or viral infections, including AIDS; the effects of radio- or
 CC chemo-therapy and Alzheimer's disease). Antagonists which bind
 CC specifically to HCNB and modulate its activity are used to treat
 CC inflammation, cancer, or immunological disorders and allograft rejection
 CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
 CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
 CC arthritis). Complement of the DNA encoding HCNB are useful as probes
 CC and primers for detecting the DNA encoding HCNB by hybridisation or
 CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
 CC particularly for diagnosis of the specified disorders, including early
 CC diagnosis of cancers. The probes can also be used to map the
 CC corresponding genomic sequence, while Ab are also useful in drug
 CC screening and for purifying native HCNB. Therapeutic agents are
 CC administered orally, intravenously, intramuscularly, topically or
 CC rectally, normally at 0.1-105 mu g.
 XX
 SQ Sequence 191 AA;
 Query Match 97.0%; Score 928; DB 19; Length 191;
 Best Local Similarity 98.4%; Pred. No. 3.2e-89;
 Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELLAEYODLFTLKOELLARRRCELLPOBORTYESSLRQVPEQILS 60
 Db 1 MGSGSRLSKELLAEYODLFTLKOELLARRRCELLPOBORTYESSLRQVPEQILS 60
 QY 61 LPELKANPEKERICRVSTSPAKDSLSEDFLDLVSFSDPATPDIKSHVAFRIPDDDD 120
 Db 61 LPELKANPEKERICRVSTSPAKDSLSEDFLDLVSFSDPATPDIKSHVAFRIPDDDD 120
 QY 121 GTLNRELSRLVNCITGEGEDTRLASSEMKNILNEESDIDRDGTINLSEFOHVISRS 180
 Db 121 GTLNRELSRLVNCITGEGEDTRLASSEMKNILNEESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSKRIYV 191
 Db 181 PDFASSKRIYV 191
 Db 181 PDFASSKRIYV 191
 RESULT 4
 AAU87324
 ID AAU87324 standard; Protein; 172 AA.
 XX AAU87324;
 AC
 XX
 DT 05-JUN-2002 (first entry)
 XX

DE Novel central nervous system protein #234.
 XX
 XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angioneuroma;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200155318-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01332.
 XX
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225265.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0225759.
 PR 22-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.

XX DE Human polypeptide SEQ ID NO 240.
XX
KW Human: antiarrhythmic; antipneumatic; antiproliferative; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; vitucide;
fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiallergic; hepatotropic; antidiabetic;
antiinflammatory; antitumor; antitumor; antitumor; antitumor;
antiparasitic; cardiant; gene therapy; cancer; immune disorder;
cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN MO20015308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184668.
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PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
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PR 01-SEP-2000; 2000US-0229287.
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PR 01-SEP-2000; 2000US-0229344.
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PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 14-SEP-2000; 2000US-0233065.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246475.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488781/53.
XX N-PSDB; AAI63868.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders -
XX
XX Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. The
XX genes were isolated from a range of human tissues disclosed in the
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
XX urogenital; (b) immune disorders e.g. Addison's disease, diabetes,
XX autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemia; and
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 184 AA;
XX
XX Query Match 39.1%; Score 374; DB 22; Length 184;
XX Best Local Similarity 43.5%; Pred. No. 4.3e-31;
XX Matches 77; Conservative 37; Mismatches 53; Indels 10; Gaps 3;
XX
XX QY 13 LAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVESSLRAQVPFEQIILSLPELKANPFKEK 72
XX DB 13 LEEYQALTLFTLRNEILCIHDTFLKCPGKYKEATL----TMDQVSSLPALRVNPFDR 68
XX QY 73 ICRVFTSPAKDSLSFEDFLDLSVSFDTATPDIKSHYAFRIEFDGDTLNREXLSRLV 132
XX DB 69 ICRVFTSPAKDSLSFEDFLDLSVSFDTATPDIKSHYAFRIEFDGDTLNREXLSRLV 125
XX
XX QY 133 NCLTGEDETRLSASEMKQLIDNILESDIDRGTINLSEFQHVIRSPDFASFKI 189
XX DB 126 LRLNSDD---MSEDLMDLTNHLVSESLDNDNMLSFSEFEHAKSPDFMNSFRI 179
XX
XX RESULT 6
XX AAB64418
XX ID AAB64418 standard; Protein; 185 AA.
XX
XX AC AAB64418;
XX
XX DT 22-MAR-2001 (first entry)
XX
XX DE Amino acid sequence of human intracellular signalling molecule INTRA50.
XX
XX KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
XX cytotatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
XX antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
XX mental disorder; schizophrenia; anxiety.
XX Homo sapiens.
XX OS
XX WO2000077040-A2.
XX
XX PD 21-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16636.
XX
XX 16-JUN-1999; 99US-0139566.
XX 17-AUG-1999; 99US-0149640.
XX 09-NOV-1999; 99US-0164417.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
XX Azimzai Y, Yang J, Reddy R, Lu DM;
XX
XX WPI; 2001-025334/03.
XX N-PSDB; AAF32687.
XX
XX New human intracellular signalling molecules, useful for the diagnosis,
XX prevention and treatment of cell proliferative, autoimmune,
XX inflammatory, neurological, gastrointestinal, reproductive and
XX developmental disorders -
XX
XX Claim 5; Page 158-159; 192pp; English.
XX
XX Sequences AAF32638 - AAF32689 represent cDNA encoding human
XX intracellular signalling molecules INTRA1 - INTRA52, represented in
XX AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
XX of the invention exhibit immunosuppressive, cytostatic, neuroprotective;
XX neotropic; antiarteriosclerotic; antifungal; anti-HIV;
XX neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
XX antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
XX agonists and antagonists are useful for the treatment of a condition
XX associated with decreased or increased expression of functional INTRA.
XX Disorders associated with abnormal INTRA expression or activity include
XX cell proliferative disorders e.g. arteriosclerosis and cancers;
XX autoimmune or inflammatory disorders e.g. Addison's disease and acquired
XX immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
XX protozoal and helminthic infections; gastrointestinal disorders e.g.
XX dysphagia and irritable bowel syndrome; neurological disorders e.g.
XX epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
XX disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
XX disorder. Antibodies immuno specific for the INTRA proteins may also be
XX useful in the diagnosis of the above disorders.
XX
XX Sequence 185 AA;
XX
XX Query Match 38.9%; Score 372; DB 22; Length 185;
XX Best Local Similarity 43.6%; Pred. No. 7.1e-31;
XX Matches 78; Conservative 36; Mismatches 55; Indels 10; Gaps 3;
XX
XX QY 11 ELLAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVESSLRAQVPFEQIILSLPELKANPFK 70
XX DB 12 EDLEEYQALTLFTLRNEILCIHDTFLKCPGKYKEATL----TMDQVSSLPALRVNPF 67
XX QY 71 ERICRVFTSPAKDSLSFEDFLDLSVSFDTATPDIKSHYAFRIEFDGDTLNREXLSRLV 130
XX DB 68 DRICRVFTSPAKDSLSFEDFLDLSVSFDTATPDIKSHYAFRIEFDGDTLNREXLSRLV 124
XX QY 131 LVNCLTGEDETRLSASEMKQLIDNILESDIDRGTINLSEFQHVIRSPDFASFKI 189
XX DB 125 IYLRNLSDD---MSEDLMDLTNHLVSESLDNDNMLSFSEFEHAKSPDFMNSFRI 180
XX
XX RESULT 7

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 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241121.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
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 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0244617.
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 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
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 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
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 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251989.
 PR 06-DEC-2000; 2000US-0251990.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251858.
 PR 08-DEC-2000; 2000US-0251859.
 PR 08-DEC-2000; 2000US-0251988.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-581633/65.
 DR N-PSDB; ABR43942.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 XX food additives or preservatives -
 PS
 XX Claim 9; SEQ ID NO 1130; 837bp; English.
 CC
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoding a
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC and angiotrophic lateral sclerosis, nervous system disorders e.g. dysphagia,
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. diabetes
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC

Query Match 36.4%; Score 348; DB 22; Length 173;
 Best Local Similarity 42.3%; Pred. No. 2.1e-28;
 Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;

QY 13 LAEYDGLFTLTKOETILAHRRFCCLLPQORVSSLRQVFEOLISPELKANPFER 72
 Db 1 LEEYQALFTLNEILCHDFTLCKPCKYKKEATL---TMDQVSSLPALRVNPFDR 56
 QY 73 ICRVSTSPADSLSEFDLILSVSDTAPPDIKSHYAFRIEDPDGTLNRELSLV 132
 Db 57 ICRVFS---HKGMFSFEDVLGMASVSEQACPSLKEIAFRITYPENGFIDEEDLQRI 113
 QY 133 NCLTGEEDTFLSASEMQLDNLIEESDIDRGITINSEFOHYISRPDPASSF 187
 Db 114 LRLNSDD---WSEDLMDLTNHLVLSXSDLDNMLSPSEFEHMAKSPDPTPF 165

RESULT 9
 AAM95362
 ID AAM95362 standard; Protein; 173 AA.
 XX
 AC AAM95362;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 XX Human reproductive system related antigen SEQ ID NO: 4020.
 DE Human reproductive system related antigen; reproductive system disorder;
 XX
 KW Human, reproductive system related antigen; reproductive system disorder;
 KW cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155320-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-0501339.
 XX

PR	31-JAN-2000;	2000US-0179065.	PR	02-OCT-2000;	2000US-0237037.
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PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249214.
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PR	01-SEP-2000;	2000US-0229343.	PR	17-NOV-2000;	2000US-0249216.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249217.
PR	01-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249218.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249244.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249245.
PR	06-SEP-2000;	2000US-0230437.	PR	17-NOV-2000;	2000US-0249264.
PR	06-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249265.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249297.
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PR	12-SEP-2000;	2000US-0231968.	PR	05-DEC-2000;	2000US-0251989.
PR	14-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251989.
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PR	25-SEP-2000;	2000US-0234998.	XX	(HUMA-) HUMAN GENOME SCI INC.	
PR	26-SEP-2000;	2000US-0235484.	XX	Rosen CA, Barash SC, Ruben SM;	
PR	27-SEP-2000;	2000US-0235834.	PI		
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PR	29-SEP-2000;	2000US-0236327.	DR	N-PSDB; AAL01332.	
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PR	29-SEP-2000;	2000US-0236368.	XX	Isolated nucleic acid molecule encoding a reproductive system antigen	
PR	29-SEP-2000;	2000US-0236369.	PT	is used in preventing, treating or ameliorating a medical condition	
PR	29-SEP-2000;	2000US-0236370.			
PR	02-OCT-2000;	2000US-0236802.			

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XX PS Claim 11; SEQ ID NO 4020; 1297pp + Sequence Listing; English.
XX CC The present invention provides the protein and coding sequences of a
XX CC number of human reproductive system related antigens. These can be used
XX CC in the prevention and treatment of reproductive system disorders,
XX CC including cancer. The present sequence is a protein of the invention.
XX SO Sequence 173 AA;

Query Match
Best Local Similarity 36.48; Score 348; DB 22; Length 173;
Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;

QY 13 LAEYDYLFLKQETLLAHRRPCCLLPQEQRTVSSSLAQQVFEQILSLPELKANPFKR 72
Db 1 LEEYQALFLTRNELLCHDTFLKCPGKYYKENTL---TMDQVSLPALRVNPFKDR 56
QY 73 ICRVSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHAFRIFFDDGTLNREXLSRLV 132
Db 57 ICRVFS---HKGMSEFEDVAGMASVSEQACPSLKITVAFRIYDFNENGFIDEDLQRII 113
QY 133 NCLTGGEDTRLASEKKQILIDNILEESDIDRGTINLSEFOHYISRSPFASPF 187
Db 114 LRLNSDD---MSEDILMDLTNHLVLSXSDLDNDNMLSFSEFHMAKSPDMPTPF 165

RESULT 10
AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX AC AAM43637;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 315.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; vitamin;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antihistaminic; antitumor; antineoplastic; anticonvulsant; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN MO200155308-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01309.
XX PR 31-JAN-2000; 2000US-0179065.
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PR 16-MAR-2000; 2000US-0189874.
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PR 19-MAY-2000; 2000US-0205515.
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PR 11-JUL-2000; 2000US-0217496.
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PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 08-NOV-2000; 2000US-0246478.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488781/53.
DR N-PSDB; AAI63943.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
XX
PS Claim 11; SEQ ID NO 315; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAI63497-AAI63660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Query Match 36.48; Score 348; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 2.1e-28;
Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;
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AC AAU19952;
XX
DT 06-DEC-2001 (first entry)
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XX Novel human calcium-binding protein #61.
XX Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide.
XX
XX Homo sapiens.
XX
PN WO200155304-A2.
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01302.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 17-MAR-2000; 2000US-0190076.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
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PR 08-NOV-2000; 2000US-0246613.
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PR 05-JAN-2001; 2001US-0255676.

(PHMA -) HUMAN GENOME SCI INC.
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PA
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PI
Rosen CA, Barash SC, Ruben SM;
WPI. 2001-465568/50.
XX
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DR
N-PSDB; AAS31637.
XX
XX
PT
Isolated nucleic acid molecule encoding a calcium-binding protein 1s
used in preventing, treating or ameliorating a medical condition -
XX
XX
PS
Claim 11; SEQ ID No 149; 542pp; English.
XX
XX
CC
The present invention relates to the isolation of novel human
CC
calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
CC
sequences encoding for these proteins. The sequences of the invention
CC
are useful in the diagnosis, prevention and/or prognosis of diseases
CC
associated with aberrant calcium flux. Such disorders include
CC
neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC
immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC
digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC
disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC
infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC
novel calcium-binding proteins are also useful as screening tools to
CC
identify antagonists and/or agonists that may enhance or inhibit
CC
activities mediated by calcium-binding proteins. The polynucleotides of
CC
the invention are also useful in gene therapy. AAU19692-AAU19699
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represent the novel human calcium-binding proteins.
CC
Note: The sequence data for this patent did not form part of the printed
CC
specification, but was obtained in electronic format directly from WIPO
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at ftp.wipo.int/pub/published_pcl_sequences.
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XX
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Query Match 36.4%; Score 348; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 2.1e-28;
Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;

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Db 1 MGSGSRLSKELLAAYQDIFLTKQELLAAHRRFCELLPQQR 43
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Search completed: January 17, 2003, 12:48:14
Job time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep: *
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep: *
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957	100.0	191	10	US-09-878-454A-2
2	945	98.7	191	12	US-10-109-885-2
3	340	35.5	187	10	US-09-802-116-2
4	185.5	19.4	170	12	US-10-109-885-3
5	178.5	18.7	195	10	US-09-999-602-3
6	173.5	18.1	195	10	US-09-999-602-4
7	142	14.8	220	10	US-09-350-874-26
8	137	14.3	216	10	US-09-350-874-6
9	137	14.3	220	10	US-09-350-874-24
10	137	14.3	227	10	US-09-350-874-8
11	137	14.3	227	10	US-09-350-874-10
12	137	14.3	245	10	US-09-350-874-4
13	137	14.3	252	10	US-09-350-874-20
14	137	14.3	270	10	US-09-350-874-14
15	136	14.2	216	9	US-09-965-528-15
16	136	14.2	216	10	US-09-350-874-2
17	135.5	14.0	214	10	US-09-999-602-1
18	134	14.0	270	10	US-09-350-874-18
19	132	13.8	225	10	US-09-350-874-30

20	132	13.8	252	10	US-09-350-874-22	Sequence 22, Appl
21	132	13.8	252	10	US-09-350-874-28	Sequence 28, Appl
22	132	13.8	252	10	US-09-350-874-42	Sequence 42, Appl
23	132	13.8	257	10	US-09-350-874-16	Sequence 16, Appl
24	122	12.7	229	10	US-09-350-874-70	Sequence 70, Appl
25	122	12.7	233	10	US-09-350-874-49	Sequence 49, Appl
26	122	12.7	233	10	US-09-350-874-49	Sequence 49, Appl
27	112.5	11.8	172	12	US-10-109-885-4	Sequence 72, Appl
28	112.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
29	112.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
30	112.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
31	112.5	11.8	1548	9	US-09-833-263-692	Sequence 692, App
32	112.5	11.8	1548	9	US-10-025-380-1095	Sequence 1095, Ap
33	111	11.6	256	10	US-09-922-217-1095	Sequence 1095, Ap
34	110.5	11.5	142	10	US-09-350-874-32	Sequence 32, Appl
35	109	11.4	642	9	US-09-910-071-4	Sequence 4, Appl
36	109	11.4	642	9	US-09-554-000-2	Sequence 2, Appl
37	109	11.4	652	9	US-09-554-000-6	Sequence 6, Appl
38	109	11.4	652	9	US-09-554-000-4	Sequence 4, Appl
39	108	11.3	256	10	US-09-554-000-8	Sequence 8, Appl
40	107.5	11.2	201	10	US-09-350-874-36	Sequence 36, Appl
41	106.5	11.1	201	10	US-09-925-297-714	Sequence 714, App
42	103	10.8	159	10	US-09-810-071-5	Sequence 5, Appl
43	101.5	10.6	203	10	US-09-350-874-12	Sequence 12, Appl
44	95.5	10.0	139	10	US-09-864-761-34808	Sequence 34808, A
45	94.5	9.9	171	9	US-09-981-353-161	Sequence 161, App
			90	10	US-09-826-589-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1:
US-09-878-454A-2
Sequence 2, Appl, Application US/09878454A
Patient No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montelito, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match	100.0%	Score 957;	DB 10;	Length 191;
Best Local Similarity	99.5%	Pred. No. 3.4e-85;		
Matches 190;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGSGSRLSKELLAEYQDLTFLTKOETLLAHRFFCLLPQEOETVSSLRAPVFFQIIS	60	
DB	1	MGSGSRLSKELLAEYQDLTFLTKOETLLAHRFFCLLPQEOETVSSLRAPVFFQIIS	60	
QY	61	LEPLKANPFRKICRYFSTSPAKDSLSFDFDLISVFSDTATPDIKSHYARIFEDDD	120	
DB	61	LEPLKANPFRKICRYFSTSPAKDSLSFDFDLISVFSDTATPDIKSHYARIFEDDD	120	
QY	121	GLTLNRXLSRLVNCITGREGEDTRLSSEKQKIDNILESDDIDROGTIMLSFQVHSRS	180	
DB	121	GLTLNRXLSRLVNCITGREGEDTRLSSEKQKIDNILESDDIDROGTIMLSFQVHSRS	180	
QY	181	PDFASSFKIVL 191		
DB	181	PDFASSFKIVL 191		

RESULT 2

US-10-109-885-2

; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; FILE REFERENCE: MODULATING CELLULAR RESPONSE TO INTERFERON
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match 98.7%; Score 945; DB 12; Length 191;
Best Local Similarity 98.4%; Pred. No. 4.9e-84;
Matches 188; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGSGRLSKELLAAYODLFTLTKQIBLLAHRRFCELLPQEQRTVSSSLRAQVPPFQILS 60
DB 1 MGGSGRLSKELLAAYODLFTLTKQIBLLAHRRFCELLPQEQRTVSSSLRAQVPPFQILS 60
QY 61 LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIFD 120
DB 61 LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIFD 120
QY 121 GTLNREXLSRLVNLCTGEGEDTFLSASEMKQLIDNILESDIDRGTINLSFQHVIRS 180
DB 121 GTLNREXLSRLVNLCTGEGEDTFLSASEMKQLIDNILESDIDRGTINLSFQHVIRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 3

US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020082406A1 Human Kinase Interacting Protein and Poly
; FILE REFERENCE: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match 35.5%; Score 340; DB 10; Length 187;
Best Local Similarity 39.9%; Pred. No. 9.7e-26;
Matches 77; Conservative 43; Mismatches 61; Indels 12; Gaps 5;

QY 1 MGGSGRLSKELLAAYODLFTLTKQIBLLAHRRFCELLPQEQRTVSSSLRAQVPPF 56
DB 1 MGNKQTVFTHEQLEAYQDCFTTFRKEIMRFLFYQDLAPQLVPLDYTTCPD---VKVPE 57
QY 57 QILSLPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIF 116
DB 58 LIGSMPELKDNPFRQIRQAQVFS-EDGCHMTLDFNLFDMFVMSMAPRDLKAYAFRIY 116
QY 117 FDDGDTLNREXLSRLVNLCTGEGEDTFLSASEMKQLIDNILESDIDRGTINLSFQHV 176
DB 117 FNNDYICAWDLEQTVTKLT-RGE---LSAEVSLVCEKVLDEADGDHGRSLSDLEFQNM 172
QY 177 ISRSPDFASSFKI 189
DB 173 ILRAPDFLSTFI 185

RESULT 4

US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; FILE REFERENCE: MODULATING CELLULAR RESPONSE TO INTERFERON
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match 19.4%; Score 185.5; DB 12; Length 170;
Best Local Similarity 31.1%; Pred. No. 6.6e-11;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIF 115
DB 41 EEFMSLPQLQNPVQVRVIDFTD-GNGEVDFKEFIEGVSVKQKQKLFARFRIY 99
QY 116 FDDGDTLNREXLSRLVNLCTGEGEDTFLSASEMKQLIDNILESDIDRGTINLSFQHV 175
DB 100 DMDKGYISNGELFQVVKMVG-----NNLKDQIQIVDKTINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 5

US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

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: CURRENT APPLICATION NUMBER: US/09/999,602
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: 09/010,378
: PRIOR FILING DATE: 1998-01-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 3
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID NO. US20020091084A1
: US-09-999-602-3

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Query Match	18.7%	Score 178.5	DB 10	Length 195
Best Local Similarity	26.7%	Pred. No. 3.8e-10		
Matches	52	Conservative	36	Mismatches 78
				Indels 29
				Gaps 6

QY 1 MGSGGSRJLK-ELLAEYODTLFLRKOEILLAHRRFCCELLPOEQRTVESSLRAQVFFEOIL 59
Db 1 MGSPASTILLRBEELIEETIKKETGFSHSDITRLRSFTSLDKGENCTLSR-----EDFQ 52
QY 60 SLPELKANPFKERICRYVSTSPAKDSLSEDFELLVSF-----SDATPDP----- 100
Db 53 RIPLELANPDLGRILNMF-PSEGGDQVNFKGFMTLHFRPIENESKIDVNGCEPINSR 111
QY 106 -IKSHVAFRIFFEDDDGTLNREKLSRLVNCITGEGEDTRLASASEKOLIDNILEESDIDR 164
Db 112 SNKTHFAFRFLRYDIDDKDKISRDDELQYLRMVG---VNISDEGLSIADRTIOEADQDG 167
QY 165 DGTINLSEFQHVYSR 179
Db 168 DSAISFEFEVAVLEK 182

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RESULT 6
US-09-999-602-4
Sequence 4, Application US/09999602
Patent No. US20020091084A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: HDVAN CALCIUM BINDING PROTEIN
FILE REFERENCE: Pf-0468-2 CON
CURRENT APPLICATION NUMBER: US/09/999,602
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/010,378
PRIOR FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO. US20020091084A1 g1706967
US-09-999-602-4

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	Query Match	18.1%	Score 173.5;	DB 10;	Length 195;
	Best Local Similarity	26.2%;	Pred. No.	1.le-09;	
	Matches 51; Conservative	36;	Mismatches	79;	Gaps 6;
OY	1 MGSQSRSLK-ELAEAYODLTFETRQELLNARRCCCLPQGQRVVESSLRQVFEEQLT	59			
Dd	1 MGSASTLLIRBDELEIEIKKETGFSHQSTRILYSRTSLSDKGENGLISR-----EDFQ	52			
OY	60 SLPEKANPFKEERICRVYSTSPAKDLSLFEDFLDLTSVF-----SDATPP-----	105			
Dd	53 RIPELLNPLODRINNAFPFE-GEQVAVFRGMRLTAHFRPLPDNEKSNDKVNGGPLPLNSR	111			

[illegible]

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1      RESULT 7
2      US-09-350-874-26
3      : Sequence 26, Application US/09350874
4      : Patent No. US20020019020A1
5      : GENERAL INFORMATION:
6      : APPLICANT: Rhodes, Kenneth
7      : APPLICANT: An, Wenqian
8      : TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
9      : FILE REFERENCE: MN1-069
10     : CURRENT APPLICATION NUMBER: US/09/350,874
11     : CURRENT FILING DATE: 1999-07-09
12     : EARLIER APPLICATION NUMBER: USSN 60/110,277
13     : EARLIER FILING DATE: 1998-11-30
14     : EARLIER APPLICATION NUMBER: USSN 60/110,033
15     : EARLIER FILING DATE: 1998-11-25
16     : EARLIER APPLICATION NUMBER: USSN 60/109,333
17     : EARLIER FILING DATE: 1998-11-20
18     : EARLIER APPLICATION NUMBER: USSN 09/298,731
19     : EARLIER FILING DATE: 1999-04-23
20     : NUMBER OF SEQ. ID NOS: 72
21     : SOFTWARE: PatentIn Ver. 2.0
22     : SEQ ID NO 26
23     : LENGTH: 220
24     : TYPE: PRT
25     : ORGANISM: Simlan sp.
26     : US-09-350-874-26

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Query Match	14.88;	Score 142;	DB 10;	Length 220;
Best Local Similarity	23.48;	Pred. No. 1.5e-06;		
Matches 43;	Conservative 46;	Mismatches 81;	Indels 14;	Gaps 5

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OY 11 ELIAYQDLFTLKEIILARRFCELLPOQRIVESSLRQVPEQLS--LEELKAMP 68
Db 41 BGLELOQJQTFTRKRELOVLYRGFKNBCP-----SGIVNEENFKQIYSQFPQGDST 93
OY 69 FKERICRYFSTSPANDSLSFEDFLDLISVFSQDFTAPOIKSHYANRIPFDDQGLINEXL 128
Db 94 YATFLFNMFQDN-HDGSVSFEFDYAGLSVIL-RGTVDRLMAWNLNLDKDGITTEEM 151
OY 129 SRLVNC---LTGEGEDTRLASAKMKQLIDNLTESDIDRGTINLSFQHYISRPFPAS 185
Db 152 LDIMKSIYDMMGKXTYPALREAPREHVENFQMKDRNKDSVYIEEFIESCQDENIMR 211
OY 186 SFKI 189
Db 212 SMOL 215

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RESULT 8
US-09-350-874-6
Sequence 6, Application US/09350874
Patent No. US20020019020A1
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: An, Wenqian
TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: NMI-069
CURRENT APPLICATION NUMBER: US/09/350,874
CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333

; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-6

Query Match 14.3%; Score 137; DB 10; Length 216;
Best Local Similarity 25.6%; Pred. No. 4.3e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;
QY 11 ELAEYQDLFLTKQETLLAHRFCCELLPOEQTVESLRAQVPEQILS--LPELKANP 68
DB 37 EGLSQLEAQNTFKRELQVLYRGFKNECP-----SGVNEETFKQIYAQFFPHGDAST 89
QY 69 FKERICRVFTSPAKDSLSPEFDLLSVFSDTATPDIKSHYAFRIEFDGDDGTLNREXL 128
DB 90 YAHYLENAFTTQT--GSVKFEDFTALSILL--RGTVHEKLRWTFNLYDINKDGVINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASEMKQLIDNILEESIDRDGTINLSEF 173
DB 148 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEF 195

RESULT 9
US-09-350-874-24
; Sequence 24, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-24

Query Match 14.3%; Score 137; DB 10; Length 220;
Best Local Similarity 22.8%; Pred. No. 4.4e-06;
Matches 42; Conservative 47; Mismatches 81; Indels 14; Gaps 5;
QY 11 ELAEYQDLFLTKQETLLAHRFCCELLPOEQTVESLRAQVPEQILS--LPELKANP 68
DB 41 EGLSQLEAQNTFKRELQVLYRGFKNECP-----SGVNEETFKQIYAQFFPHGDAST 93
QY 69 FKERICRVFTSPAKDSLSPEFDLLSVFSDTATPDIKSHYAFRIEFDGDDGTLNREXL 128
DB 94 YATFLNFAFTN--HDGVSFEDFVAGLSVIL--RGTVDRLNWFNLYDINKDGCITKEEM 151
QY 129 SRLVNC---LTGEGEDTRLASEMKQLIDNILEESIDRDGTINLSEFQHVSRSPDFAS 185
DB 152 LDINKSIYDMGKYTPALREAPREHVESFFQKMDKNKDGIVTLDEF 211
QY 186 SFKI 189
; :

DB 212 SMQL 215

RESULT 10
US-09-350-874-8
; Sequence 8, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-350-874-8

Query Match 14.3%; Score 137; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 4.6e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;
QY 11 ELAEYQDLFLTKQETLLAHRFCCELLPOEQTVESLRAQVPEQILS--LPELKANP 68
DB 48 EGLEQLAQNTFKRELQVLYRGFKNECP-----SGVNEETFKQIYAQFFPHGDAST 100
QY 69 FKERICRVFTSPAKDSLSPEFDLLSVFSDTATPDIKSHYAFRIEFDGDDGTLNREXL 128
DB 101 YAHYLENAFTTQT--GSVKFEDFTALSILL--RGTVHEKLRWTFNLYDINKDGVINKEEM 158
QY 129 SRLVNC---LTGEGEDTRLASEMKQLIDNILEESIDRDGTINLSEF 173
DB 159 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEF 206

RESULT 11
US-09-350-874-10
; Sequence 10, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-10


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Db 144 YATFLNADTN-HDGSVSFEDEFVAGLSVIL-RGTVDDLWAFNLYDLNRKDCGCTKEEM 201
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHVISRSPDFAS 185
Db 202 LDIMKSIYDMGKYTPYPALREAPREHVESFFQKMDRKNKGWVTTEEFTEESQCKDENMR 261
QY 186 SPKI 189
Db 262 SMQL 265

```

RESULT 15

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US-09-965-528-15
; Sequence 15, Application US/09965528
; Publication NO. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda M.
; APPLICANT: LO, Dzung Alina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 3216587CD1
US-09-965-528-15

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Query Match 14.2%; Score 136; DB 9; Length 216;
Best Local Similarity 25.6%; Pred. No. 5.4e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELIAEQDLTFLKQELLAHRRFCELLPQEQRTVESSLRAQVPPFQILS--LPELKAMP 68
Db 37 EGLEQLEAQTNFTKRELQVLYRGFKNECP-----SGVVEDTFKQIYAQFPFHGDAST 89
QY 69 FKERICRVFTSPAKDSLSEFDELDSLVSFDTATPDIKSHYAFRIFDFDDGTLNREXL 128
Db 90 YAHVLFNAFTTQT-GSVKFEDEFVATLSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEF 173
Db 148 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEF 195

```

Search completed: January 17, 2003, 12:50:14
Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:47:19 : Search time 17 Seconds

(Without alignments)
1080.099 Million cell updates/sec

Title: MUT127

Perfect score: 957

Sequence: 1 MGSGSRLSKELLAEYQDLT.....EPQHVSRSPDFASPKRIVL 191

Scoring table: BLOSUM62DX 1
Gapop 10.0, Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database:

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	408	42.6	311	2	T21563	hypothetical prote
2	209.5	21.9	174	2	T41632	probable calcineu
3	203.5	21.3	175	2	JH0462	phosphoprotein pho
4	198.5	20.7	174	2	T47245	calcineurin regula
5	185.5	19.4	170	1	A33391	calcineurin regula
6	185.5	19.4	170	1	S34127	calcineurin regula
7	185.5	19.4	170	1	JC1220	calcineurin regula
8	185.5	19.4	216	1	S42716	calcineurin regula
9	182.5	19.1	369	2	T22708	calcineurin regula
10	177.5	18.5	170	2	JC5174	hypothetical prote
11	174.5	18.2	170	2	JC7242	calcineurin regula
12	173.5	18.1	170	2	A44307	calcineurin regula
13	171.5	17.9	179	2	JC1221	calcineurin regula
14	169.5	17.7	165	2	PS0261	calcineurin regula
15	169.5	17.7	176	2	JQ1232	calcineurin regula
16	169.5	17.7	195	2	T28047	calcineurin regula
17	169.5	17.7	213	2	T31775	hypothetical prote
18	165.5	17.3	190	2	T20725	hypothetical prote
19	163.5	17.1	226	2	T51357	hypothetical prote
20	155	16.2	190	2	I51686	calcineurin B-like
21	151.5	15.8	226	2	T08923	calcineurin B-like
22	150.5	15.7	213	2	T51356	calcineurin B-like
23	150	15.7	193	2	JH0816	calcineurin B-like
24	150	15.7	193	2	I50676	neural vistin-like
25	150	15.7	246	2	T05308	gene Rem-1 protein
26	150	15.7	246	2	H85387	hypothetical prote
27	149	15.6	193	2	S47565	hypothetical prote
28	147	15.4	192	2	T01375	calcium-binding prote
29	144	15.0	190	2	A55666	calcium sensor hom
						neurocalcin - frul

30	141	14.7	191	2	JH0815	neural vistin-lik
31	137.5	14.4	254	2	T29566	hypothetical prote
32	137	14.3	193	2	JC2186	hypocalcin - huma
33	137	14.3	270	2	JC7631	K+ channel-interac
34	136	14.2	224	2	F96668	protein F1N19.5 [1
35	134	14.0	193	2	JH0616	neurocalcin (clone
36	134	14.0	195	2	JC1347	hypocalcin - rat
37	133	13.9	190	2	S58303	related to neurona
38	132	13.8	191	2	JH0605	neural vistin-lik
39	132	13.8	191	2	A48979	visinin-lik prote
40	130.5	13.6	172	2	S38531	catractin - mouse
41	129	13.5	791	2	A53691	diacylglycerol kin
42	128	13.4	190	2	S61168	hypothetical prote
43	127.5	13.3	172	2	I38424	centrin - human
44	126	13.2	214	2	T08922	hypothetical prote
45	125.5	13.1	202	2	S21155	recoverin - mouse

ALIGNMENTS

RESULT 1
T21563
Hypothetical protein F30A10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21563
R:Barlow, K.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19442
A:Accession: T21563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-311 <NTL>
A:Cross-references: EMBL:Z81072; PDB:CAE03019.1; GSPDB:GN00019; CESP:F30A10.1
A:Experimental source: clone F30A10
A:Genetic: CESP:F30A10.1
A:Gene: CESP:F30A10.1
A:Map position: 1
A:Introns: 106/2; 139/3; 190/3; 240/1

Query Match 42.6%; Score 408; DB 2; Length 311;
Best Local Similarity 42.0%; Pred. No. 6.4e-24;
Matches 87; Conservative 42; Mismatches 52; Indels 26; Gaps 5;

QY 1 MGSGSRLS-----KELLAEYQDLTFTKBEILLAHRRPELLPQKRTYESS 48
DB 111 MGNASSLSLEINLFSKGVFTREGLDYODCTFTFRDITRLKRYALNPHK---VPTN 167
QY 49 LRAQVP-----FEQILSLPELKNPFRICRVSPAKDSIFEDFLDSFSDTA 102
DB 168 MGRRPALITLTFPEVAKMEIKNPKRRCICEFS-EDGRGNISFDFLDMSVSEMA 226
QY 103 TPDIKSYARIDEFDDGTLNREXLSRLVNCITGEGEDFRLASAKKOLIDNLEESDT 162
DB 227 PLQIKLKYAFRIYDDELGHDLDSKMRSLTRD---ELSDVEVEFITERIERADL 282
QY 163 DRDGTINLSEFOHVSRSPDFASPKR 189
DB 283 DGDSINFAFEFHVSRSPDFIRFHT 309

RESULT 2
T41632
Probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C:Accession: T41632
R:MDougal, R.M.; Rajadream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
Submitted to the EMBL Data Library, August 1999
A:Reference number: Z22005
A:Accession: T41632
A:Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA
A; Residues: 1-175 <MAI>
A; Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL
R; Experimental source: strain S288C
R; Wieman, S.; Voss, H.; Schwagerl, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grotj
submitted to the EMBL Data Library, July 1993
A; Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosom
A; Reference number: S34679
A; Accession: S34680
A; Molecule type: DNA
A; Residues: 31-175 <WI2>
A; Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235
A; Experimental source: strain S288C
R; Pardo, J.M.
submitted to the EMBL Data Library, September 1993
A; Description: The protein phosphatase calcineurin is essential for NaCl tolerance i
A; Reference number: S52281
A; Accession: S52282
A; Molecule type: DNA
A; Residues: 1-175 <PAR>
A; Cross-references: EMBL:Z36521; NID:g473144; PIDN:CAA81290.1; PID:g473146
C; Genetics:
A; Gene: SGD:CNI1; YCN2
A; Cross-references: SGD:S0001673; MIPS:YKL190W
A; Map position: III
A; Introns: 18/1
C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; I/I
F; 2-175/Product: phosphoprotein phosphatase regulatory chain #status: predicted <MAY
F; 21-52/Domain: calmodulin repeat homology <EF1>
F; 53-85/Domain: calmodulin repeat homology <EF2>
F; 90-122/Domain: calmodulin repeat homology <EF3>
F; 131-163/Domain: calmodulin repeat homology <EF4>
F; 2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

Query Match 21.3%; Score 203.5; DB 2; Length 175;
Best Local Similarity 27.1%; Pred. No. 1.2e-08;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRSLRLAEAYODLFLTKQETLLAHRRFCPELLPQRTVSSLRQAQVPFEQILS 60
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1 MGAAPSKIIVDGLLED----TNFDREIERLRKRFMKLD RDSSSIDKN-----EFMS 48
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

QY 61 LPELKANPFKRICRVFTSPAKDSLSFEDLLLSVFSDTATPDIKSHVAFRIFFDDDD 120
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 49 IPGVSSNPLAGRIMEVFDADNSGD-VDFQEFITGLSFISGRGSKDEKLRAFKIYIDKD 107
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

QY 121 GTLNREXLSRLVNCLTGEGEDTRLASEMKOLINDILEESDDRGTINISEQHVI 177
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 108 GFISNGELFVLKIMVG----SNLIDBQLQIIVDRITVENDSGDGRLSPFEFNKAI 160
::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

RESULT 4
T47245
calcineurin regulatory chain [imported] - Neurospora crassa
C; Species: Neurospora crassa
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C; Accession: T47245
R; Dieminger, M.; Tropischug, M.
submitted to the EMBL Data Library, April 1997
A; Reference number: Z24421
A; Accession: T47245
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-174 <DIE>
A; Cross-references: EMBL:X12814; PIDN:CAA73345.1
A; Experimental source: strain 74 A
C; Genetics:
A; Gene: Can B
C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: EF hand

Query Match 20.7%; Score 198.5; DB 2; Length 174;

Best Local Similarity 26.1%; Pred. No. 2.9e-08;
Matches 41; Conservative 42; Mismatches 61; Indels 13; Gaps 3;

OY 24 KOELLAHRECELLPEOQTVESLSAQVFEIILSPELKANPEKRICRVSTSPAK 83
DB 20 REEDVLRKRFMKDKNSGTIER-----EEFLSPQISTNPPLATRMIAIDENGCG 71
OY 84 DSLSEFEDLDLVSFSTAPADPKSHAFRPFDDGDTINREXLSLVNCLGEGEDTR 143
DB 72 D-VDFPEVSGLSAFSKGKKEOKLRFAFYVDIDRDGYISNGELFTVLKMGV-----SN 126
OY 144 LSASEMKQILDNIIESDIDRDGTINLSEFOHVISRS 180
DB 127 LKDOQLORIVDKTIMEDLDKCKISFEFTKVENT 163

RESULT 5

A33391
calcineurin regulatory chain - human
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
A:Accession: A33391
R:Guertin, D.; Krinks, M.H.; Sikelja, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A:Reference number: A33391; MUID:90126237; PMID:255868
A:Accession: A33391
A:Molecule type: mRNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M30773; NID:9180704; PIDN:AA808721.1; PID:9180705
C:Genetics:
A:Gene: GDB:PPP3R1; CALNB
A:Cross-references: GDB:136804; OMIM:601302
A:Map position: 2p16-2p15
A:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:3/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (asn) #status predicted
F:31.33.35.37.42/Binding site: calcium (asp, asp, ser, ser, glu) #status predicted
F:63.65.67.69.74/Binding site: calcium (asp, asp, asn, glu, glu) #status predicted
F:100.102.104.106.111/Binding site: calcium (asp, asp, asp, tyr, glu) #status predicted
F:141.143.145.147.152/Binding site: calcium (asp, asp, asp, arg, glu) #status predicted

Query Match 19.4%; Score 185.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 2.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

OY 56 EQLSLPELKANPEKRICRVSTSPAKDSLSEFEDLDLVSFSTAPADPKSHAFRIF 115
DB 41 EEFMSLPQLQNPVLRVIDIDFTD-GNGEVDKFEFIEGVSOFSYKGDKEOKLRFAFRIF 99
OY 116 DFDDGDTINREXLSRLVNCITGEGEDTRLASSEMQLIDNIIESDIDRDGTINLSEFOH 175
DB 100 DMDKDGYSNGELFQVLKMGV-----NNLKDTQLQIYDKTITINDKDGKISFEFPCA 155
OY 176 VI 177
DB 156 VV 157

RESULT 6

S34127
calcineurin regulatory chain (validated) - bovine
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C:Accession: I45831; J10297; S34127
R:Nargang, C.E.; Bottoiff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994

A:Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A:Reference number: I45831; MUID:95102111; PMID:7603816
A:Accession: I45831
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <NA2>
A:Cross-references: EMBL:X71666; NID:9312968; PIDN:CAA50659.1; PID:9312969
R:Altken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A:Title: The structure of the B subunit of calcineurin.
A:Reference number: J10297; MUID:84132092; PMID:6321184
A:Accession: J10297
A:Molecule type: protein

A:Residues: 2-11, 'M', '13-153', 'S', '155-169' <AIT>
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Shtuchak, M.D.; Thomson, J.A.; Fitzgibbon, submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66708; PDB:1TGO
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Shtuchak, M.D.; Thomson, J.A.; Fitzgibbon, Cell 82, 507-522, 1995

A:Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant cyclosporin A
A:Reference number: A56967; MUID:95360994; PMID:7543369
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status experimental <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:3/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F:3/Modified site: aspartic acid (asn) #status predicted
F:31.33.35.37.42/Binding site: calcium (asp, asp, ser, ser, glu) #status experimental
F:63.65.67.69.74/Binding site: calcium (asp, asp, asn, glu, glu) #status experimental
F:100.102.104.106.111/Binding site: calcium (asp, asp, asp, tyr, glu) #status experimental
F:141.143.145.147.152/Binding site: calcium (asp, asp, asp, arg, glu) #status experimental

Query Match 19.4%; Score 185.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 2.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

OY 56 EQLSLPELKANPEKRICRVSTSPAKDSLSEFEDLDLVSFSTAPADPKSHAFRIF 115
DB 41 EEFMSLPQLQNPVLRVIDIDFTD-GNGEVDKFEFIEGVSOFSYKGDKEOKLRFAFRIF 99
OY 116 DFDDGDTINREXLSRLVNCITGEGEDTRLASSEMQLIDNIIESDIDRDGTINLSEFOH 175
DB 100 DMDKDGYSNGELFQVLKMGV-----NNLKDTQLQIYDKTITINDKDGKISFEFPCA 155
OY 176 VI 177
DB 156 VV 157

RESULT 7

JC1220
calcineurin regulatory chain, brain - mouse
N:Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: J1220
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.; Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A:Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase
A:Reference number: J1220; MUID:9239379; PMID:1325794
A:Accession: J1220
A:Molecule type: mRNA
A:Residues: 1-170 <UDE>
A:Cross-references: GB:S43864; NID:9255078; PIDN:AA823171.1; PID:9255079

A;Experimental source: brain
C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneural functions.
C;Genetics:
A;Gene: PP2B-beta-1
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipophilic

F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 19.4%; Score 185.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 2.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

Qy 56 EQILSLPELKANPKFKRICRVFTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
 |:|::|||:: || :| :: | :|::|: || :| :|::|: |
Db 41 EEFMSLPELQQNPLVQRVIDIFTD-GNGEVDFKEFGVSQVKGDKEQLRFARFIY 99

Qy 116 DFDDDGTLNRXLSRLNYCLTGEGEDPRLSASEMKQLINDLEESDIDRDGTINLSEFH 175

Db 100 DMDKDGYISNGELFQVLKMVG-----NNLDKTQLQIVDKTIINADKGGRISFFEECA 155

Qy 176 VI 177
 |:|
Db 156 VV 157

RESULT 8
S42716
M;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphate-binding protein
N;Contains: calcineurin regulatory chain, short splice form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S42716; S42717
E;Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
Biochim. Biophys. Acta 1217, 174-180, 1994
A;Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of calcineurin
A;Reference number: S42716; MID:94153993; PMID:8110831
A;Accession: S42716
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-216 <CHAI>
A;Cross-references: EMBL:D14425; NID:g286205; PIDN:BAA03318.1; PID:g286206
A;Accession: S42717
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-216 <CHAI>
A;Cross-references: EMBL:D14568; NID:g286255; PIDN:BAA03422.1; PID:g286256
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipophilic

F;2-170/Product: calcineurin regulatory chain, long splice form #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: aspartic acid (Asn) #status predicted

Query Match 19.4%; Score 185.5; DB 1; Length 216;
Best Local Similarity 31.1%; Pred. No. 3.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

Qy 56 EQILSLPELKANPKFKRICRVFTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
 |:|::|||:: || :| :: | :|::|: || :| :|::|: |
Db 87 EEFMSLPELQQNPLVQRVIDIFTD-GNGEVDFKEFGVSQVKGDKEQLRFARFIY 145

